OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:52:57 ; Search time 1530 Seconds
(without alignments)
201.120 Million cell updates/sec

Title: US-09-856-662-3
Perfect score: 19
Sequence: 1 tacatggacaacacgcagt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: [illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	372	12	BF714056	BF714056 ma[illegible]
	2	19	100.0	841	13	BI111603	BI111603 602895964
	3	17.4	91.6	112	12	BF117527	BF117527 [illegible]
c	4	17.4	91.6	132	13	BG982142	BG982142 CM4-CN009
	5	17.4	91.6	154	12	BF915646	BF915646 IL3-UT011
	6	17.4	91.6	155	12	BF174345	BF174345 MYE3014 M
	7	17.4	91.6	165	9	AA066306	AA066306 mm08e07.r
c	8	17.4	91.6	165	13	BI107895	BI107895 [illegible]
	9	17.4	91.6	170	10	BE478050	BE478050 16212? BA
	10	17.4	91.6	172	12	BF893661	BF893661 QV1 MT016
	11	17.4	91.6	184	9	AA358919	AA358919 EST67850
	12	17.4	91.6	184	14	BM846913	BM846913 K EST[illegible]
	13	17.4	91.6	193	12	BF025999	BF025999 [illegible]
	14	17.4	91.6	198	10	BE486556	BE486556 174621 BA
	15	17.4	91.6	201	14	BM754247	BM754247 K EST[illegible]
	16	17.4	91.6	201	17	AZ104395	AZ104395 [illegible]K22
	17	17.4	91.6	205	12	BF452043	BF452043 [illegible]
	18	17.4	91.6	206	14	BM842838	BM842838 K EST[illegible]
	19	17.4	91.6	207	10	BE482618	BE482618 [illegible] BA
	20	17.4	91.6	208	10	BE480250	BE480250 165268 BA
	21	17.4	91.6	208	12	BF353880	BF353880 [illegible]
	22	17.4	91.6	209	12	BG687764	BG687764 [illegible] BA
	23	17.4	91.6	209	12	BG693552	BG693552 343826 BA
	24	17.4	91.6	209	14	F06589	F06589 HSC1DF031 n
	25	17.4	91.6	210	12	BG693126	BG693126 [illegible] BA
	26	17.4	91.6	212	12	BG693402	BG693402 [illegible] BA
	27	17.4	91.6	217	14	BM820355	BM820355 K EST0088
	28	17.4	91.6	221	12	BF230591	BF230591 25235[illegible] BA
	29	17.4	91.6	222	10	BE477008	BE477008 16[illegible]512 BA
	30	17.4	91.6	222	10	BE481198	BE481198 16654[illegible] BA
	31	17.4	91.6	222	12	BF342889	BF342889 602015180
	32	17.4	91.6	223	12	BF914950	BF914950 IL3-[illegible]
	33	17.4	91.6	225	10	BE486303	BE486303 17[illegible]887 BA
	34	17.4	91.6	233	10	BE588315	BE588315 194175 BA
c	35	17.4	91.6	234	12	BE839129	BE839129 [illegible]
	36	17.4	91.6	235	12	BF913002	BF913002 MR3-[illegible]
	37	17.4	91.6	236	10	BE589294	BE589294 195370 BA
	38	17.4	91.6	240	10	BE481116	BE481116 166430 BA
	39	17.4	91.6	240	12	BF176369	BF176369 MYE[illegible] M
	40	17.4	91.6	242	14	BM740411	BM740411 K EST0011
	41	17.4	91.6	243	10	BE486467	BE486467 174418 BA
	42	17.4	91.6	243	14	BM847721	BM847721 K EST[illegible]
	43	17.4	91.6	244	9	AA160070	AA160070 [illegible]
	44	17.4	91.6	246	10	BE476956	BE476956 160434 BA
	45	17.4	91.6	247	10	BE477249	BE477249 [illegible] BA

ALIGNMENTS

RESULT 1
BF714056
LOCUS BF714056 372 bp mRNA linear EST [illegible] JAN [illegible]
DEFINITION ma509f02.x1 Soares_NMEBA_branchial arch Mus musculus cDNA clone IMAGE:3969915 3' similar to TR:O19440 O19440 MAJOR HISTOCOMPATIBILITY COMPLEX CLASS [illegible] mRNA sequence.
ACCESSION BF714056
VERSION BF714056.1 GI:12013328
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 372)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo , Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
[illegible]/resources.shtml

MGI:1469947

```
            Possible reversed clone: similarity on wrong strand
            High quality sequence stop: 362.
FEATURES             Location/Qualifiers
     source          1..372
                     /organism "Mus musculus"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:[illegible]"
                     /clone_lib "Soares NMEBA branchial arch"
                     /tissue_type "branchial arches"
                     /dev_stage "embryo, 10.5 dpc"
                     /lab_host "DH10B (phage resistant)"
                     /note "Vector: pT7T3D Pac (Pharmacia) with a modified
                     polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     [illegible]TTTTTTTTTTTTTTTTTTTT
                     3'], double stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT       84 a    105 c    120 g     63 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 1[illegible];  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              |||||||||||||||||||
Db         [illegible] TACGTGGACAACACGCAGT [illegible]


RESULT 2
BF1[illegible]
LOCUS       BF1[illegible]                 841 bp    mRNA    linear   EST 26-JUN-2001
DEFINITION  [illegible] NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:[illegible] 5',
            mRNA sequence.
ACCESSION   BF1[illegible]
VERSION     BF1[illegible].1  GI:[illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 841)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM[illegible] row: [illegible] column: [illegible]
            High quality sequence stop: 8[illegible].
FEATURES             Location/Qualifiers
     source          1..841
                     /organism "Mus musculus"
                     /strain "C57BL/6J"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:[illegible]"
                     /clone_lib "NCI_CGAP_Mam5"
                     /tissue_type "tumor, gross tissue"
                     /dev_stage "7 months"
                     /lab_host "DH10B"
                     /note "Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
                     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
BASE COUNT      174 a    237 c    271 g    159 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 13;  Length 841;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              |||||||||||||||||||
Db        277 TACGTGGACAACACGCAGT 295


RESULT 3
BF117527
LOCUS       BF117527                 112 bp    mRNA    linear   EST 29-DEC-2000
DEFINITION  uz38b03.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3671309 5'
            similar to TR:Q61642 Q61642 HISTOCOMPATIBILITY 2, K REGION
            PRECURSOR ;, mRNA sequence.
ACCESSION   BF117527
VERSION     BF117527.1  GI:10987003
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 112)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml

            MGI:1432077
            Trace considered overall poor quality
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..112
                     /organism "Mus musculus"
                     /strain "C57BL/6J"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:3671309"
                     /clone_lib "NCI_CGAP_Mam5"
                     /tissue_type "tumor, gross tissue"
                     /dev_stage "7 months"
                     /lab_host "DH10B"
                     /note "Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
                     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH"
BASE COUNT       18 a     36 c     40 g     18 t
ORIGIN

  Query Match             91.6%;  Score 17.4;  DB 12;  Length 112;
  Best Local Similarity   94.7%;  Pred. No. 1e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              |||||||||||||| ||||
Db         92 TACGTGGACAACACGGAGT 110


RESULT 4
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BG982142/c
LOCUS       BG982142               132 bp    mRNA    linear   EST 12-JUN-2001
DEFINITION  CM4 CN0090 130201 722 d08 CN0090 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG982142
VERSION     BG982142.1  GI:14384877
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 132)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            http://www.ludwig.org.br/scripts/getfasta2.pl?id=CM4&id2=CM4-CN0090
            130201-722-d08&t3=2001-02-13&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 6
            High quality sequence stop: 130.
FEATURES             Location/Qualifiers
     source          1..132
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CN0090"
                     /dev_stage="Adult"
                     /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716    Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       24 a     44 c     42 g     22 t
ORIGIN

  Query Match             91.6%;  Score 17.4;  DB 12;  Length 132;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGGCAGT 19
              |||||||| ||||||||||
Db         62 TACGTGGACGACACGGCAGT 44


RESULT 5
BF915646
LOCUS       BF915646               154 bp    mRNA    linear   EST 18-JAN-2001
DEFINITION  IL3-UT0114-061200-373-E01 UT0114 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF915646
VERSION     BF915646.1  GI:12307104
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 154)
```

```
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            http://www.ludwig.org.br/scripts/getfasta2.pl?id=IL3&id2=IL3-UT0114
            061200-373-E01&t3=2000-12-06&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 31
            High quality sequence stop: 154.
FEATURES             Location/Qualifiers
     source          1..154
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="UT0114"
                     /dev_stage="Adult"
                     /note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716    Ludwig Institute for Cancer Research)
                     profiles into  the puc 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       34 a     40 c     61 g     19 t
ORIGIN

  Query Match             91.6%;  Score 17.4;  DB 12;  Length 154;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGGCAGT 19
              |||||||| ||||||||||
Db         28 TACGTGGACGACACGGCAGT 46


RESULT 6
BF174345
LOCUS       BF174345               155 bp    mRNA    linear   EST 27-MAR-2001
DEFINITION  MYE3014 Myeloma (MYE) cDNA library, Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BF174345
VERSION     BF174345.1  GI:13440559
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 155)
  AUTHORS   Claudio,J.O., Tang,H., Khan,E.M., Voralia,M., Li,Z., Sukernik,E.,
            Francisco,Catalan,A., Liew,C.C. and Stewart,A.K.
  TITLE     The transcriptional phenotype of myeloma cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: A. Keith Stewart, M.D.
            Oncology Research
            University Health Network
            610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
            Tel: (416) 946-4539
            Fax: (416) 946-6546
```

```
                Email: k.stewart@utoronto.ca
                PCR PRimers
                FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG-3'
                BACKWARD: 5' CTAGTGAATTGTAATACGACTCACTATAGGGCG-3'
                Seq primer: 5' GAAATTAACCCTCACTAAAGG-3'.
FEATURES             Location/Qualifiers
     source          1..155
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Myeloma (MYP) cDNA library"
                     /sex="Male"
                     /tissue_type="Blood"
                     /cell_type="myeloma"
                     /dev_stage="multiple myeloma"
                     /note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2:
                     XhoI; Myeloma cells from multiple myeloma patients' bone
                     marrow were purified by  magnetic cell sorting. mRNA were
                     purified and an oligo d(T)18 primer  containing XhoI
                     restriction site was used to prime first strand synthesis
                     using M-MLV reverse transcriptase. To protect the cDNAs
                     from XhoI digestion  in subsequent cloning step, the
                     nucleotide analogue 5-methyl dCTP was added  to the
                     nucleotide mixture and [a-32P]dATP was added to monitor
                     the quantity  and quality of first strand synthesis. After
                     second strand synthesis and  blunting of cDNA termini,
                     EcoRI adapters were ligated, followed by kinase  treatment
                     and digestion with XhoI. The cDNAs were then
                     size fractionated  using Sephacryl S-500 column and then
                     ligated into EcoRI and XhoI digested  Lambda Zap Express
                     vector. The ligation product was packaged using Gigapack
                     II packaging extract. The library had primary titre of
                     approx. 1x10^6. Clones from  the primary library were
                     randomly selected for single pass sequencing."
BASE COUNT       32 a     49 c     62 g     12 t
ORIGIN

  Query Match             91.6%;  Score 17.4;  DB 12;  Length 155;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              ||||  || | ||||||||
Db         67 TACTGGACGACACGCAGT 85


RESULT 7
AA066306
LOCUS       AA066306                 165 bp    mRNA    linear   EST 04-FEB-1997
DEFINITION  mm06e07.r1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
            clone IMAGE:520092 5' similar to gb:M11284 Mouse MHC class I Q4 Ha
            mRNA. (MOUSE);, mRNA sequence.
ACCESSION   AA066306
VERSION     AA066306.1  GI:1563376
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 165)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:314780
            Seq primer: -28M13 rev2 ET from Amersham
            High quality sequence stop: 137.
FEATURES             Location/Qualifiers
     source          1..165
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:520092"
                     /clone_lib="Stratagene mouse diaphragm (#937303)"
                     /tissue_type="diaphragm"
                     /dev_stage="adult"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
                     prepared from diaphragm muscle.  Primer: Oligo dT. Average
                     insert size: 1.5 kb. Uni-ZAP XR Vector;  5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3'  3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTTTT 3'"
BASE COUNT       23 a     61 c     44 g     37 t
ORIGIN

  Query Match             91.6%;  Score 17.4;  DB 9;  Length 165;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              ||||||||| |||||||||
Db        135 TACGTGGACGACACGCAGT 153


RESULT 8
BI107895/c
LOCUS       BI107895                 165 bp    mRNA    linear   EST 26-JUN-2001
DEFINITION  602961843F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5031599 5'
            mRNA sequence.
ACCESSION   BI107895
VERSION     BI107895.1  GI:14558788
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 165)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu Xia Deng Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11088  row: e  column: 12
            High quality sequence stop: 165.
FEATURES             Location/Qualifiers
     source          1..165
                     /organism="Mus musculus"
                     /strain="129/C57BL/6J,FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5031599"
                     /clone_lib="NCI_CGAP_Mam3"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="10 months"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Chu Xia Deng, NIH
```

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            Reference for transgenic model: Xu et al., Nature Genetics
            22, 37-43 (1999)."
BASE COUNT       31 a     50 c     55 g     29 t
ORIGIN

  Query Match              91.6%;  Score 17.4;  DB 13;  Length 165;
  Best Local Similarity    94.7%;  Pred. No. 1.2e-02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGGCAGT 19
              |||||||| |||||||||
Db         63 TACGTGGACGACACGGCAGT 45


RESULT 9
BE478659
LOCUS       BE478659                170 bp    mRNA    linear   EST 28-AUG-2000
DEFINITION  192107 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE478659
VERSION     BE478659.1  GI:9597583
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 170)
  AUTHORS   Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and
            Wells,K.D.
  TITLE     Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@anri.barc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 5  row: M  column: 10
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1..170
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="BARC 5BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled mRNA isolated from mammary
                     tissues at eight physiological, developmental, and disease
                     states."
BASE COUNT       18 a     63 c     53 g     36 t
ORIGIN

  Query Match              91.6%;  Score 17.4;  DB 10;  Length 170;
  Best Local Similarity    94.7%;  Pred. No. 1.2e-02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGGCAGT 19
              |||||||| |||||||||
Db        143 TACGTGGACGACACGGCAGT 161


RESULT 10
BF893661
LOCUS       BF893661                172 bp    mRNA    linear   EST 18-JAN-2001
DEFINITION  QV1-MT0167-131100-485-h11 MT0167 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF893661
VERSION     BF893661.1  GI:12285029
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 172)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=QV1&t2=QV1-MT0167
            -131100-485-h11&t3=2000-11-13&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 8
            High quality sequence stop: 171.
FEATURES             Location/Qualifiers
     source          1..172
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MT0167"
                     /dev_stage="Adult"
                     /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 - Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT       24 a     53 c     57 g     38 t
ORIGIN

  Query Match              91.6%;  Score 17.4;  DB 12;  Length 172;
  Best Local Similarity    94.7%;  Pred. No. 1.2e-02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGGCAGT 19
              |||||||| |||||||||
Db        125 TACGTGGACGACACGGCAGT 143


RESULT 11
AA358919
LOCUS       AA358919                184 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST67858 Fetal lung II Homo sapiens cDNA 5' end similar to similar
            to major histocompatibility complex, class I, HLA-E, mRNA
            sequence.
ACCESSION   AA358919
VERSION     AA358919.1  GI:2011249
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 184)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
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            Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
            O., Sutton,G., Blake,J.A., Brandon,R.C., Man Wai,C., Clayton,R.A.,
            Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald
            ,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
            Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S. Jr., Kelley,J.M.,
            Kelley,J.C., Liu,L.I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.
            , Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
            Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
            Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
            ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
            Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
COMMENT     Other ESTs: THC169519
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018690423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1..184
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):105..."
                     /db_xref="taxon:9606"
                     /clone_lib="Fetal lung II"
                     /sex="male"
                     /dev_stage="fetus, 16 wks."
                     /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
                     ; Site_2: XhoI"
BASE COUNT       25 a     66 c     56 g     32 t     5 others
ORIGIN

  Query Match             91.6%;  Score 17.4;  DB 6;  Length 184;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              |||||||||| ||||||||
Db        162 TACGTGGACGACACGCAGT 180


RESULT 12
BM849913
LOCUS       BM849913                 184 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0126021 S13KMS5 Homo sapiens cDNA clone S13KMS5-45-G10 5',
            mRNA sequence.
ACCESSION   BM849913
VERSION     BM849913.1  GI:19263312
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 184)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 45  row: G  column: 10
            High quality sequence stop: 184.
FEATURES             Location/Qualifiers
     source          1..184
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S13KMS5-45-G10"
                     /clone_lib="S13KMS5"
                     /tissue_type="myeloma"
                     /cell_line="KMS-5"
                     /lab_host="Top10F'"
                     /note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
                     (A)+ RNA was dephosphorylated with bacterial alkaline
                     phosphatase (BAP) and then decapped with tabacco acid
                     pyrophosphatase (TAP). The decapped intact mRNA was
                     ligated with DNA-RNA linker including EcoR I site by
                     treatment of T4 RNA ligase and the first strand cDNA was
                     synthesized from oligo-dT selected mRNA by priming with
                     dT tailed vector. The dT tailed vector was adjusted to
                     have about 60nt. The cDNA vector was circularized with E.
                     coli DNA ligase after digestion of EcoRI which site is
                     also included in vector. An RNA strand converted to a DNA
                     strand by Okayama-Berg method. The obtained cDNA vectors
                     were used for transformation of competent cells E. coli
                     Top10F' by electroporation method. The cDNA libraries
                     constructed by this method are full length enriched cDNA
                     library."
BASE COUNT       31 a     57 c     68 g     28 t
ORIGIN

  Query Match             91.6%;  Score 17.4;  DB 14;  Length 184;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              ||||||||| |||||||||
Db         81 TACGTGGACGACACGCAGT 99


RESULT 13
BF025999
LOCUS       BF025999                 193 bp    mRNA    linear   EST 16-OCT-2000
DEFINITION  601670466F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3953401 5',
            mRNA sequence.
ACCESSION   BF025999
VERSION     BF025999.1  GI:10733711
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 193)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/NIH/DIP
            cDNA Library Preparation: Life Technologies/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM824  row: k  column: 02
            High quality sequence stop: 191.
FEATURES             Location/Qualifiers
     source          1..193
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                          /organism="Homo sapiens"
                          /db_xref="taxon:9606"
                          /clone="IMAGE:3953401"
                          /clone_lib="NIH_MGC_20"
                          /tissue_type="melanotic melanoma"
                          /lab_host="DH10B (phage-resistant)"
                          /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                          EcoRI; cDNA made by oligo-dT priming. Directionally
                          cloned into EcoRI/XhoI sites using the following 5'
                          adaptor: GGCACGAG(G). Size-selected >500bp for average
                          insert size 1.8kb. Library constructed by Ling Hong in
                          the laboratory of Gerald M. Rubin (University of
                          California, Berkeley) using ZAP cDNA synthesis kit
                          (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT       27 a     67 c     67 g     31 t      1 others
ORIGIN

  Query Match              91.6%;  Score 17.4;  DB 12;  Length 193;
  Best Local Similarity    94.7%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGGCAGT 19
              |||||||| ||||||||||
Db        123 TACGTGGACGACACGGCAGT 141


RESULT 14
BE486556
LOCUS       BE486556                 198 bp    mRNA    linear   EST 28-AUG-2000
DEFINITION  174621 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE486556
VERSION     BE486556.1  GI:9606089
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 198)
  AUTHORS   Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and
            Wells,K.D.
  TITLE     Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@anri.barc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: CTTTTCCCAGTCACGACG
            Plate: 127  row: B  column: 12
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1..198
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="BARC 5BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled mRNA isolated from mammary
                     tissues at eight physiological, developmental, and disease
                     states."
BASE COUNT       28 a     70 c     61 g     39 t
ORIGIN

  Query Match              91.6%;  Score 17.4;  DB 10;  Length 198;
  Best Local Similarity    94.7%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGGCAGT 19
              |||||||| ||||||||||
Db        140 TACGTGGACGACACGGCAGT 158


RESULT 15
BM754247
LOCUS       BM754247                 201 bp    mRNA    linear   EST 4-MAR-2002
DEFINITION  K-EST0031533 S2SNU668s1 Homo sapiens cDNA clone S2SNU668s1-7-G05
            5', mRNA sequence.
ACCESSION   BM754247
VERSION     BM754247.1  GI:19083865
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 201)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Cho,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 7  row: G  column: 05
            High quality sequence stop: 201.
FEATURES             Location/Qualifiers
     source          1..201
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S2SNU668s1-7-G05"
                     /clone_lib="S2SNU668s1"
                     /sex="M"
                     /tissue_type="Ascites"
                     /cell_type="Epithelial"
                     /cell_line="SNU-668"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was decapped with tabacco
                     acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
                     including EcoRI site by treatment of T4 RNA ligase. The
                     first strand cDNA was synthesized from oligo dT selected
                     mRNA by priming with dT tailed vector. The dT tailed
                     vector was adjusted to have about 60nt. The cDNA vector
                     was circularized with E. coli DNA ligase after digestion
                     of EcoRI which site is also included in vector. An RNA
                     strand converted to a DNA strand by Okayama-Berg method.
                     The obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     After analyzing and sequencing about 2,000 - 3,000
                     colonies in original cDNA library, the abundant cDNAs were
                     selected and amplified by PCR reaction using vector region
                     primer including T7 promotor as 5' primer and N(dT)14 as
                     3' primer. The PCR products were used as template for
                     synthesis of biotinylated single stranded RNA by in vitro
                     transcription reaction. The synthesized RNA probes were
                     hybridized with antisense single stranded cDNAS prepared
                     from original liberary and incubated with avidin gel.
                     After removing DNA-RNA hybrids by centrifuge, the
                     subtracted cDNA libraries were constructed by
                     transformaion of the remaining DNA into competent cells E.
                     coli Top10F' with electroporation method."
BASE COUNT       38 a     56 c     74 g     33 t
ORIGIN
```

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  Query Match             91.6%;  Score 17.4;  DB 14;  Length 201;
  Best Local Similarity   94.7%;  Pred. No. [illegible];
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACTTGGACAACAGGCAGT 19
              ||||||||| |||||||||
Db         23 TACTTGGACGACAGGCAGT 41

Search completed: April 15, 2003, [illegible]
Job time : [illegible] secs
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:1[illegible]:22 ; Search time 214 Seconds
(without alignments)
199.9[illegible] Million cell updates/sec

Title: US-09-856-662-3
Perfect score: 19
Sequence: 1 tacgtggacaacacgcagt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: [illegible]_NA19[illegible].DAT:*
2: [illegible]_NA19[illegible].DAT:*
3: [illegible]_NA19[illegible].DAT:*
4: [illegible]_NA19[illegible].DAT:*
5: [illegible]_NA1984.DAT:*
6: [illegible]_NA1985.DAT:*
7: [illegible]_NA1986.DAT:*
8: [illegible]_NA1987.DAT:*
9: [illegible]_NA1988.DAT:*
10: [illegible]_NA1989.DAT:*
11: [illegible]_NA1990.DAT:*
12: [illegible]_NA1991.DAT:*
13: [illegible]_NA1992.DAT:*
14: [illegible]_NA1993.DAT:*
15: [illegible]_NA1994.DAT:*
16: [illegible]_NA1995.DAT:*
17: [illegible]_NA1996.DAT:*
18: [illegible]_NA1997.DAT:*
19: [illegible]_NA1998.DAT:*
20: [illegible]_NA1999.DAT:*
21: [illegible]_NA2000.DAT:*
22: [illegible]_NA2[illegible]A.DAT:*
23: [illegible]_NA2[illegible]B.DAT:*
24: [illegible]_NA2[illegible].DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	19	21	AAA66945	Human leukocyte an
	2	17.4	91.6	153	23	AAS83588	DNA encoding novel
	3	17.4	91.6	153	23	AAS86539	DNA encoding novel
	4	17.4	91.6	268	18	AAV02693	Human Class I non-
	5	17.4	91.6	270	20	AAZ79222	HLA allele B*[illegible]
	6	17.4	91.6	270	20	AAZ79272	HLA allele B*1406
	7	17.4	91.6	270	21	AAA94616	HLA-A gene exon 2
	8	17.4	91.6	270	21	AAA94612	HLA-B gene exon 2
	9	17.4	91.6	270	21	AAA94615	HLA-C gene exon 2
	10	17.4	91.6	270	21	AAA11077	Consensus sequence
c	11	17.4	91.6	270	22	ABA47215	Human breast cell
c	12	17.4	91.6	270	22	ABA65099	Human foetal liver
c	13	17.4	91.6	270	22	ABA32204	Probe #10670 for d
c	14	17.4	91.6	270	22	AAK13521	Human brain expres
c	15	17.4	91.6	270	22	AAK[illegible]260	Human bone marrow
c	16	17.4	91.6	270	22	AAI20871	Probe #10[illegible]04 for d
c	17	17.4	91.6	270	22	AAI45269	Probe #1[illegible]955 used
c	18	17.4	91.6	270	22	AAI05778	Probe #5769 used t
c	19	17.4	91.6	270	24	ABL[illegible]345	Human genome-deriv
	20	17.4	91.6	271	21	AAA94617	HLA-A gene exon 2
	21	17.4	91.6	351	24	ABA98516	Human leukocyte an
	22	17.4	91.6	385	21	AAA94621	HLA-C gene exon 2
	23	17.4	91.6	405	24	ABK54010	Human head and ne
	24	17.4	91.6	429	22	AAH35452	Human colon cancer
	25	17.4	91.6	436	24	ABA98543	Human leukocyte an
c	26	17.4	91.6	439	22	ABA42060	Human breast cell
c	27	17.4	91.6	439	22	ABA52481	Human foetal liver
c	28	17.4	91.6	439	22	ABA22273	Probe #739 for det
c	29	17.4	91.6	439	22	AAK00748	Human brain expres
c	30	17.4	91.6	439	22	AAK26200	Human bone marrow
c	31	17.4	91.6	439	22	AAI10831	Probe #764 for det
c	32	17.4	91.6	439	22	AAI32089	Probe #779 used to
c	33	17.4	91.6	439	22	AAI00756	Probe #747 used to
c	34	17.4	91.6	439	24	ABS00786	Human genome-deriv
	35	17.4	91.6	447	21	AAC03768	Human secreted pro
	36	17.4	91.6	453	24	ABA98517	Human leukocyte an
	37	17.4	91.6	460	23	AAS83589	DNA encoding novel
	38	17.4	91.6	468	20	AAZ07237	Human lung tumour
	39	17.4	91.6	468	21	AAC79127	Human lung tumour
	40	17.4	91.6	[illegible]	[illegible]	AA[illegible]	Human lung tumour-
	41	17.4	91.6	[illegible]	[illegible]	AAC03769	Human secreted pro
	42	17.4	91.6	[illegible]	[illegible]	AA[illegible]	DNA #[illegible] encoding
	43	17.4	91.6	[illegible]	[illegible]	AAC00214	Human secreted pro
	44	17.4	91.6	618	[illegible]	AA[illegible]	DNA encoding novel
	45	17.4	91.6	[illegible]	[illegible]	AA[illegible]	DNA encoding novel

ALIGNMENTS

RESULT 1
AAA66945
ID AAA66945 standard; DNA; 19 BP.
XX
AC AAA66945;
XX
DT [illegible] (first entry)
XX
DE Human leukocyte antigen A allele DNA probe A[illegible] SEQ ID NO:3.
XX
KW Human leukocyte antigen; HLA; class I allele type; probe; PCR primer;
KW amplification; hybridisation; organ transplant; gene typing;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO200031295-A1.
XX
PD 02-JUN-2000.
XX
PF 07-OCT-1999; 99WO-JP05527.
XX
PR 26-NOV-1998; 98JP-0335151.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Moribe T, Kaneshige T;
XX
DR WPI; 2000-400057/34.
XX
PT Simple, rapid and accurate method for distinguishing HLA class I allele
PT type with possibility of mechanization and automation, applicable in

PT Subtract donor recipient compatibility during organ transplant and
PT disease diagnosis
XX
PS Claim 8; Page 50; 85pp; Japanese.
XX
CC the present invention describes a method for distinguishing a human
CC leukocyte antigen (HLA) class I antigen or allele by a combination
CC of polymerase chain reaction (PCR) using a primer pair whereby all
CC HLA A, B or C alleles can be amplified or using reverse hybridisation
CC analysis comprising a DNA probe covalently bonded to microtitre plate
CC wells which are hybridisable specifically with the base sequence of at
CC least one specific HLA A, B or C allele. The method is applicable in
CC gene typing, subtract donor recipient compatibility during organ
CC transplant and correlation analysis for diagnosis of various diseases.
CC The method is simple, rapid and accurate, with possibility of
CC mechanisation and automation, without the problems encountered by using
CC the prior art techniques. AAA66943 to AAA67072 represent oligonucleotide
CC probes and PCR primers for use in the method of the present invention..
XX
SQ Sequence 150 BP; 6 A; 5 C; 5 G; 8 T; 0 other;

Query Match 100.0%; Score 19; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TACTGTGGACAACACGCAGT 19
||||||||||||||||||||
Db 1 TACTGTGGACAACACGCAGT 19

RESULT 2
AAS86588
ID AAS86588 standard; cDNA; 153 BP.
XX
AC AAS86588;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19492.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0644167.
XX
PA (HYSE) HYSEQ INC.
XX
PI Drmanac R, Labat C, Lapat Y;
XX
DR WPI; 2001-638362/73.
DR P-PSDB; AB022252.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID No 19492; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantifating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity,
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64167 AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 153 BP; 27 A; 55 C; 46 G; 25 T; 0 other;

Query Match 91.6%; Score 17.4; DB 23; Length 153;
Best Local Similarity 94.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACTGTGGACAACACGCAGT 19
||||||||||||||||||||
Db 78 TACTGTGGACGACACGCAGT 96

RESULT 3
AAS86589
ID AAS86589 standard; cDNA; 153 BP.
XX
AC AAS86589;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #22454.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0644167.
XX
PA (HYSE) HYSEQ INC.
XX
PI Drmanac R, Labat C, Lapat Y;
XX
DR WPI; 2001-638362/73.
DR P-PSDB; AB022252.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID No 22454; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197 AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC N Terminal: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 153 BP; 27 A; 55 C; 46 G; 25 T; 0 other;

Query Match 91.6%; Score 17.4; DB 23; Length 153;
Best Local Similarity 94.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||||||| ||||||||||
Db 78 TACGTGGACGACACGCAGT 96

RESULT 4
AAV02693
ID AAV02693 standard; DNA; 268 BP.
XX
AC AAV02693;
XX
DT 19-MAY-1998 (first entry)
XX
DE Human Class I non-classical HLA gene exon 2 consensus DNA.
XX
KW Human leukocyte antigen class I gene, non-classical HLA, allele testing,
KW donor; tissue matching; recipient, graft rejection; class typing; ds.
XX
OS Homo sapiens.
XX
PN WO9723645 A1.
XX
PD 03-JUL-1997.
XX
PF 04-JAN-1996; 96WO-US00362.
XX
PR 04-JAN-1996; 96WO-US00362.
XX
PA (SLOA) SLOAN KETTERING INST CANCER RES.
XX
PI Cereb N, Yang SY;
XX
DR WPI; 1997-351080/32
XX
PT DNA based human leukocyte antigen class I gene typing method
PT useful for tissue matching and prevention of graft versus host
PT disease
XX
PS Disclosure; Fig 6; 99pp; English.
XX
CC AAV02693 is a consensus sequence of the human leukocyte antigen (HLA)
CC Class I non-classical HLA genes exon 2, which is used in a novel method
CC for testing a tissue sample to determine the allelic type of a HLA class
CC I gene in the sample. The HLA Class I gene is selected from among HLA-A,
CC -B and -C genes. The method comprises of treating the tissue sample to
CC obtain nucleic acid polymers suitable for amplification then combining
CC these polymers with a first primer which hybridises with a portion of
CC intron 1 or intron 3 of the HLA Class I gene and a second primer which
CC hybridises with a different portion of the HLA Class I gene under
CC conditions suitable for amplification to obtain an amplified product.
CC The product is then evaluated to determine the allelic type of the
CC HLA-Class I gene. The method is useful for tissue matching HLA class I
CC antigens between donors and recipients and hence for preventing graft
CC versus host disease.
XX
SQ Sequence 268 BP; 52 A; 86 C; 92 G; 36 T; 2 other;

Query Match 91.6%; Score 17.4; DB 19; Length 268;
Best Local Similarity 94.7%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||||||| ||||||||||
Db 78 TACGTGGACGACACGCAGT 96

RESULT 5
AAZ39222
ID AAZ39222 standard; DNA; 270 BP.
XX
AC AAZ39222;
XX
DT 11-FEB-2000 (first entry)
XX
DE HLA allele B*3913 exon 2 sequence.
XX
KW Human leukocyte antigen; HLA; allele; HLA-B*3913; HLA-B*1409; human;
KW HLA-B*51; HLA DRB1*0820; HLA-DRB1*04; HLA-DRB4*01; allele typing; ex a;
KW major histocompatibility complex; MHC; ss.
XX
OS Homo sapiens.
XX
PN WO9954496 A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-EP02614.
XX
PR 20-APR-1998; 98EP-0870088.
XX
PA (INNO) INNOGENETICS NV
XX
PI De Canck I, Mersch G, Kosser R;
XX
DR WPI; 1999-664608/54.
DR P-PSDB; AAY59742.
XX
PT New polynucleotides for human leukocyte antigen, HLA, allele fragments,
PT useful for typing HLA alleles
XX
PS Claim 12; Page 11; 62pp; English.
XX
CC The invention provides polynucleotides derived from exon 2 and exon 3
CC of human leukocyte antigen (HLA) alleles HLA B*3913, HLA B*1409 and
CC HLA B*51 and exon 2 of HLA alleles HLA DRB1*0820, HLA-DRB1*04 and
CC HLA-DRB4*01. The polynucleotides are useful for typing the above HLA
CC alleles in a sample, especially by a method that comprises (a) amplifying
CC all/part of the relevant sequence using at least one primer pair; and (b)
CC hybridizing the amplified product to a set of probes specifically
CC hybridizing to target regions comprising one or more polymorphic
CC nucleotides of the sequence, to determine the absence or presence of the
CC allele in the sample. Diagnostic kits for (a) typing the alleles
CC comprising at least one preferred primer and/or at least one preferred
CC probe and (b) for detecting the protein fragment encoded by the
CC polynucleotides comprising an antibody or fragment (e.g. antibody)
CC binding specifically to the protein fragment are provided. The
CC polynucleotides also enable the isolation of the complete respective
CC genes from a human genomic library.
XX
SQ Sequence 270 BP; 58 A; 85 C; 90 G; 37 T; 0 other;

Query Match 91.6%; Score 17.4; DB 20; Length 270;
Best Local Similarity 94.7%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| ||||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 6
AAA94612
ID   AAA94612 standard; DNA; 270 BP.
XX
AC   AAA94612;
XX
DT   11 JAN 2001  (first entry)
XX
DE   HLA A gene exon 2 #1.
XX
KW   Human leukocyte Antigen; HLA A; antigen presentation; HLA typing;
KW   organ transplantation; autoimmune disease;
KW   infectious disease susceptibility; chromosome 6p21.3; ds.
XX
OS   Homo sapiens.
XX
PN   US6103465-A.
XX
PD   15 AUG 2000.
XX
PF   03-OCT-1995;  95US-005 06666.
XX
PR   14 FEB 1995;  95US-039 02551.
XX
PA   (PEKF ) PERKIN ELMER CORP.
XX
PI   Parham P;  Johnston Dow T;  Chadwick BS;
XX
DR   WPI; 2000-512544/49.
XX
PT   Typing HLA class I genes for organ transplantation, involves contacting
PT   the sample DNA containing HLA class I gene comprising two exons and a
PT   target sequence, with amplification primers and detecting the amplicon
PT
XX
PS   Example 2; Fig 5; 60pp; English.
XX
CC   The present sequence is exon 2 of Human Leukocyte Antigen-A (HLA A) gene.
CC   HLA A gene is found on chromosome 6p21.3. HLA class I proteins are found
CC   on the surface of almost all nucleated cells and are involved in antigen
CC   presentation to immune system cells. This sequence was used in the method
CC   of the present invention, in which primers are used to type HLA class I
CC   genes, by carrying out PCR on a sample DNA, comprising HLA class I gene,
CC   and detecting the amplicon formed using a sequence specific detection
CC   method e.g. DNA sequencing. The method of the present invention is useful
CC   for discriminating among the HLA A, HLA B, and HLA C genes and other
CC   related class I genes and pseudogenes. In addition, the method of the
CC   present invention is useful for organ transplantation studies, for the
CC   study of autoimmune disease and for the determination of susceptibility
CC   to infectious disease.
XX
SQ   Sequence 270 BP; 56 A; 84 C; 93 G; 37 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 21;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| ||||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 8
AAA94612
ID   AAA94612 standard; DNA; 270 BP.
XX
AC   AAA94612;
XX
DT   11 JAN 2001  (first entry)
XX
DE   HLA B gene exon 2 #1.
XX
KW   Human leukocyte Antigen; HLA B; antigen presentation; HLA typing;
KW   organ transplantation; autoimmune disease;
KW   infectious disease susceptibility; chromosome 6p21.3; ds.
XX
OS   Homo sapiens.
```

```
XX
PN   US6103465-A.
XX
PD   15-AUG-2000.
XX
PF   03-OCT-1995;   95US-0538666.
XX
PR   14-FEB-1995;   95US-0390251.
XX
PA   (PERE ) PERKIN-ELMER CORP.
XX
PI   Parham P, Johnston-Dow L, Chadwick RB;
XX
DR   WPI; 2000-542544/49.
XX
PI   Typing HLA class I genes for organ transplantation, involves contacting
PI   the sample DNA containing HLA class I gene comprising two exons and a
PT   target sequence, with amplification primers and detecting the amplicon
PT   .
XX
PS   Example 2; Fig 11; 60pp; English.
XX
CC   The present sequence is exon 2 of Human leukocyte Antigen-B (HLA-B) gene.
CC   HLA-B gene is found on chromosome 6p21.3. HLA class I proteins are found
CC   on the surface of almost all nucleated cells and are involved in antigen
CC   presentation to immune system cells. This sequence was used in the method
CC   of the present invention, in which primers are used to type HLA class I
CC   genes: by carrying out PCR on a sample DNA, comprising HLA class I gene,
CC   and detecting the amplicon formed using a sequence-specific detection
CC   method e.g. DNA sequencing. The method of the present invention is useful
CC   for discriminating among the HLA-A, HLA-B, and HLA-C genes and other
CC   related class I genes and pseudogenes. In addition, the method of the
CC   present invention is useful for organ transplantation studies, for the
CC   study of autoimmune disease and for the determination of susceptibility
CC   to infectious disease.
XX
SQ   Sequence 270 BP; 60 A; 85 C; 90 G; 35 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 21;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      79 TACGTGGACGACACGCAGT 97


RESULT 9
AAA94615
ID   AAA94615 standard; DNA; 270 BP.
XX
AC   AAA94615;
XX
DT   11-JAN-2001  (first entry)
XX
DE   HLA-C gene exon 2 #1.
XX
KW   Human leukocyte Antigen; HLA-C; antigen presentation; HLA typing;
KW   organ transplantation; autoimmune disease;
KW   infectious disease susceptibility; chromosome 6p21.3; ds.
XX
OS   Homo sapiens.
XX
PN   US6103465-A.
XX
PD   15-AUG-2000.
XX
PF   03-OCT-1995;   95US-0538666.
XX
PR   14-FEB-1995;   95US-0390251.
XX
PA   (PERE ) PERKIN-ELMER CORP.
XX
PI   Parham P, Johnston-Dow L, Chadwick RB;
XX
DR   WPI; 2000-542544/49.
XX
PT   Typing HLA class I genes for organ transplantation, involves contacting
PT   the sample DNA containing HLA class I gene comprising two exons and a
PT   target sequence, with amplification primers and detecting the amplicon.
PT   .
XX
PS   Example 2; Fig 19; 60pp; English.
XX
CC   The present sequence is exon 2 of Human leukocyte Antigen-C (HLA-C) gene.
CC   HLA-C gene is found on chromosome 6p21.3. HLA class I proteins are found
CC   on the surface of almost all nucleated cells and are involved in antigen
CC   presentation to immune system cells. This sequence was used in the method
CC   of the present invention, in which primers are used to type HLA class I
CC   genes, by carrying out PCR on a sample DNA, comprising HLA class I gene,
CC   and detecting the amplicon formed using a sequence-specific detection
CC   method e.g. DNA sequencing. The method of the present invention is useful
CC   for discriminating among the HLA-A, HLA-B, and HLA-C genes and other
CC   related class I genes and pseudogenes. In addition, the method of the
CC   present invention is useful for organ transplantation studies, for the
CC   study of autoimmune disease and for the determination of susceptibility
CC   to infectious disease.
XX
SQ   Sequence 270 BP; 54 A; 85 C; 99 G; 32 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 21;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 16
AAA11077
ID   AAA11077 standard; DNA; 270 BP.
XX
AC   AAA11077;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Consensus sequence for exon 2 of non classical HLA genes.
XX
KW   tissue sample testing; allelic typing; human leukocyte antigen;
KW   PCR primer; probe; hybridisation; intron; amplification; ds;
KW   allelic variation; non-classical HLA class I gene; exon.
XX
OS   Homo sapiens.
XX
PN   US6010775-A.
XX
PD   29-FEB-2000.
XX
PF   22-DEC-1995;   95US-0577081.
XX
PR   22-DEC-1995;   95US-0577081.
XX
PA   (CERE/) CEREB N.
PA   (YANG/) YANG S Y.
XX
PI   Cereb N, Yang SY;
XX
DR   WPI; 2000-224159/19.
XX
PT   Testing a tissue sample to determine the allelic type of a human
PT   leukocyte antigen class I gene comprises amplification of nucleic acid
PT   polymers with primers which flank a region including an allelic
PT   variation of the HLA class I gene.
XX
PS   Disclosure; Column 51-52; 90pp; English.
```

```
XX
CC   The invention relates to a method (i) for testing a tissue sample to
CC   determine the allelic type of a human leukocyte antigen (HLA) class I
CC   gene in the sample, where the HLA class I gene is selected from HLA-A,
CC   HLA-B or HLA-C, by: (a) treating the tissue sample to obtain nucleic
CC   acid polymers suitable for amplification; (b) combining the nucleic acid
CC   polymers with a primer which hybridizes with a portion of intron 1 or
CC   intron 3 of the HLA class I gene, and a second primer which hybridizes
CC   with a different portion of the HLA class I gene and performing
CC   amplification, where the primers flank a region including at least one
CC   site of allelic variation in at least one of exons 2 or 3 of the HLA
CC   class I gene and where the first primer is a locus specific primer which
CC   hybridizes with intron 1 or 3 of only one of the HLA class I genes; and
CC   (c) evaluation the amplified product to determine the allelic type of
CC   the HLA class I gene. The method is useful for testing a tissue sample
CC   to determine the allelic type of a classical or non-classical HLA class
CC   I gene in the sample. The sequences AAAiio3 Allaz represent consensus
CC   sequences of introns and exons of the HLA genes and primers and probes
CC   used to isolate and analyze the HLA genes.
XX
SQ   Sequence 270 BP; 56 A; 80 C; 92 G; 30 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 21;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db     78 TACGTGGACGACACGCAGT 96


RESULT 11
ABA47215/c
ID   ABA47215 standard; DNA; 270 BP.
XX
AC   ABA47215;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human breast cell single exon nucleic acid probe #5010.
XX
KW   Human; microarray; single exon probe; gene expression; breast;
KW   disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180512.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236459.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE ) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG, Hanzel DK, Chen W, Kank DR;
XX
DR   WPI; 2001-470033/51.
XX
PT   New spatially addressable set of single exon nucleic acid probes,
PT   useful for measuring gene expression in sample derived from human
PT   breast, comprises number of single exon nucleic acid probes.
XX
PS   Claim 1; SEQ ID NO 5010; 6.7pp; sequence listing; English.
XX
CC   The invention relates to a spatially addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human breast and BT 474 cells. The method involves contacting
CC   the probes with a collection of detectably labelled nucleic acids
CC   derived from mRNA of human breast, and then measuring the label
CC   bound to each probe of the microarray. The probes are useful for
CC   verifying the expression of regions of genomic DNA predicted to
CC   encode proteins. They are useful for gene discovery, and for
CC   determining predisposition and/or prognosis of breast disease. Gene
CC   expression analysis is useful for assessing the toxicity of chemical
CC   agents on cells. The microarray of this invention presents a far greater
CC   diversity of probes for measuring gene expression, with far less bias
CC   than expressed sequence tag microarrays. The method is suitable for
CC   rapid production of functional information from genomic sequence. The
CC   present sequence is a single exon nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from Wilo at http.wipo.int/pub/published.pct sequences.
XX
SQ   Sequence 270 BP; 56 A; 94 C; 85 G; 36 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 22;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db     193 TACGTGGACGACACGCAGT 175


RESULT 12
ABA65009/c
ID   ABA65009 standard; DNA; 270 BP.
XX
AC   ABA65009;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #13404.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180512.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236459.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE ) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG, Hanzel DK, Chen W, Kank DR;
XX
DR   WPI; 2001-470033/51.
XX
PT   Human genome derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human foetal liver
XX
PS   Claim 4; SEQ ID NO 13404; 6.6pp; sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   foetal liver. The present sequence is a single exon nucleic acid
```

```
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 270 BP; 35 A; 94 C; 85 G; 56 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 22;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||| ||||||||||
Db     193 TACGTGGACGACACGCAGT 175


RESULT 13
ABA32204/C
ID   ABA32204 standard; DNA; 270 BP.
XX
AC   ABA32204;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Probe #10670 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180412.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE ) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DK;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analysing gene expression in human
PT   hearts -
XX
PS   Claim 4; SEQ ID No 10670; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 270 BP; 35 A; 94 C; 85 G; 56 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 22;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||| ||||||||||
Db     193 TACGTGGACGACACGCAGT 175


RESULT 14
AAK13521/C
ID   AAK13521 standard; DNA; 270 BP.
XX
AC   AAK13521;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 10512
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180412.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE ) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DK;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analysing gene expression in human
PT   brains
XX
PS   Example 4; SEQ ID NO: 10512; 65pp - Sequence Listing: English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 270 BP; 35 A; 94 C; 85 G; 56 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 22;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||| ||||||||||
Db     193 TACGTGGACGACACGCAGT 175


RESULT 15
AAK39260/C
ID   AAK39260 standard; DNA; 270 BP.
XX
AC   AAK39260;
```

```
XX
DT   06 NOV 2001  (first entry)
XX
DE   Human bone marrow expressed single exon probe SEQ ID NO: 13817.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-[illegible]
PR   [illegible]
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-480000/53.
XX
PT   Human genome derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human bone marrow
XX
PS   Example 4; SEQ ID NO 13817; 658pp; Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC   the probes of the invention.
XX
SQ   Sequence 270 BP; 35 A; 94 C; 85 G; 56 T; 0 other;

  Query Match             91.6%;  Score 17.4;  DB 22;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 20;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          [illegible]
Db      [illegible]


Search completed: April 15, 2003, [illegible]
Job time : [illegible]
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GenCore version 5.1.4.p5_4578

oM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:54:37 ; Search time 89 Seconds
(without alignments)
65.470 Million cell updates/sec

Title: US-09-856-662-3
Perfect score: 19
Sequence: 1 tacgtgacaacacgcagt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441562 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 992724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iss_PC/*.seq:*
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5: /cgn2_6/ptodata/1/iss_PE/*.seq:*
6: /cgn2_6/ptodata/1/iss_backfiles1.seq:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17.4	91.6	270	1	US-08-127-954-53	Sequence 53, Appl
2	17.4	91.6	270	1	US-08-127-954-54	Sequence 54, Appl
3	17.4	91.6	270	1	US-08-127-954-55	Sequence 55, Appl
4	17.4	91.6	270	1	US-08-127-954-56	Sequence 56, Appl
5	17.4	91.6	270	1	US-08-127-954-57	Sequence 57, Appl
6	17.4	91.6	270	1	US-08-127-954-58	Sequence 58, Appl
7	17.4	91.6	270	1	US-08-127-954-59	Sequence 59, Appl
8	17.4	91.6	270	1	US-08-127-954-60	Sequence 60, Appl
9	17.4	91.6	270	1	US-08-127-954-61	Sequence 61, Appl
10	17.4	91.6	270	1	US-08-127-954-62	Sequence 62, Appl
11	17.4	91.6	270	1	US-08-127-954-63	Sequence 63, Appl
12	17.4	91.6	270	1	US-08-127-954-64	Sequence 64, Appl
13	17.4	91.6	270	1	US-08-127-954-65	Sequence 65, Appl
14	17.4	91.6	270	1	US-08-127-954-66	Sequence 66, Appl
15	17.4	91.6	270	1	US-08-127-954-67	Sequence 67, Appl
16	17.4	91.6	270	1	US-08-127-954-68	Sequence 68, Appl
17	17.4	91.6	270	1	US-08-127-954-69	Sequence 69, Appl
18	17.4	91.6	270	1	US-08-127-954-70	Sequence 70, Appl
19	17.4	91.6	270	1	US-08-127-954-71	Sequence 71, Appl
20	17.4	91.6	270	1	US-08-127-954-72	Sequence 72, Appl
21	17.4	91.6	270	1	US-08-127-954-73	Sequence 73, Appl
22	17.4	91.6	270	1	US-08-127-954-74	Sequence 74, Appl
23	17.4	91.6	270	1	US-08-127-954-75	Sequence 75, Appl
24	17.4	91.6	270	1	US-08-127-954-76	Sequence 76, Appl
25	17.4	91.6	270	1	US-08-127-954-77	Sequence 77, Appl
26	17.4	91.6	270	1	US-08-127-954-78	Sequence 78, Appl
27	17.4	91.6	270	1	US-08-127-954-79	Sequence 79, Appl
28	17.4	91.6	270	1	US-08-127-954-80	Sequence 80, Appl
29	17.4	91.6	270	1	US-08-127-954-81	Sequence 81, Appl
30	17.4	91.6	270	1	US-08-127-954-82	Sequence 82, Appl
31	17.4	91.6	270	1	US-08-127-954-83	Sequence 83, Appl
32	17.4	91.6	270	1	US-08-127-954-84	Sequence 84, Appl
33	17.4	91.6	270	1	US-08-127-954-85	Sequence 85, Appl
34	17.4	91.6	270	1	US-08-127-954-86	Sequence 86, Appl
35	17.4	91.6	270	1	US-08-127-954-87	Sequence 87, Appl
36	17.4	91.6	270	1	US-08-127-954-88	Sequence 88, Appl
37	17.4	91.6	270	1	US-08-127-954-89	Sequence 89, Appl
38	17.4	91.6	270	1	US-08-127-954-90	Sequence 90, Appl
39	17.4	91.6	270	1	US-08-127-954-91	Sequence 91, Appl
40	17.4	91.6	270	1	US-08-127-954-92	Sequence 92, Appl
41	17.4	91.6	270	1	US-08-127-954-93	Sequence 93, Appl
42	17.4	91.6	270	3	US-08-577-081A-39	Sequence 39, Appl
43	17.4	91.6	466	4	US-09-039-838-155	Sequence 155, App
44	17.4	91.6	1183	3	US-09-029-045-11	Sequence 11, Appl
c 45	15.8	83.2	4059	2	US-08-564-614-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-127-954-53
; Sequence 53, Application US/08127954
; Patent No. 5451512
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Bunawan, Teodorica L.
; APPLICANT: [illegible], Henry A.
; TITLE OF INVENTION: Methods and Reagents for HLA Class I A
; TITLE OF INVENTION: Locus DNA Typing
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,954
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,421
; REFERENCE/DOCKET NUMBER: 3973
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-127-954-53

Query Match 91.6%; Score 17.4; DB 1; Length 270;
Best Local Similarity 94.7%; Pred. No. 2.6;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGACAACACGCAGT 19
|||||||||| ||||||||||
Db 78 TACGTGACAACACGCAGT 96

```
RESULT 2
US-08-127-954-54
; Sequence 54, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Bugawan, Teodorica L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,954
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8073
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-127-954-54

  Query Match             91.6%;  Score 17.4;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              |||||||| ||||||||||
Db         78 TACGTGGACGACACGCAGT 96


RESULT 3
US-08-127-954-55
; Sequence 55, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Bugawan, Teodorica L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,954
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8073
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-127-954-55

  Query Match             91.6%;  Score 17.4;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
              |||||||| ||||||||||
Db         78 TACGTGGACGACACGCAGT 96


RESULT 4
US-08-127-954-56
; Sequence 56, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Bugawan, Teodorica L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,954
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8073
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  DNA (genomic)
US-08-127-954-56

  Query Match             91.6%;  Score 17.4;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 5
US-08-127-954-57
; Sequence 57, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Buqawan, Teodorica L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,954
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,421
;      REFERENCE/DOCKET NUMBER:  8874
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-127-954-57

  Query Match             91.6%;  Score 17.4;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 6
US-08-127-954-58
; Sequence 58, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Buqawan, Teodorica L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,954
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,421
;      REFERENCE/DOCKET NUMBER:  8874
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-127-954-58

  Query Match             91.6%;  Score 17.4;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 7
US-08-127-954-59
; Sequence 59, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Buqawan, Teodorica L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,954
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,421
```

```
;       REFERENCE/DOCKET NUMBER:  8873
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 814 2974
;       TELEFAX:  (510) 814 2977
;   INFORMATION FOR SEQ ID NO:  59:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  270 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-127-954-59

  Query Match             91.6%;  Score 1234;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches  180;  Conservative    0;  Mismatches    11;  Indels    0;  Gaps    0;

Qy       1 TAGTGGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TAGTGGGACAGACACGCAGT 97


RESULT 8
US-08-127-954-60
; Sequence 60, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Bugawan, Teodorico L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110 1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,954
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,821
;      REFERENCE/DOCKET NUMBER:  8873
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814 2974
;      TELEFAX:  (510) 814 2977
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-127-954-60

  Query Match             91.6%;  Score 1234;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches  180;  Conservative    0;  Mismatches    11;  Indels    0;  Gaps    0;

Qy       1 TAGTGGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TAGTGGGACAGACACGCAGT 97


RESULT 9
US-08-127-954-61
; Sequence 61, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Bugawan, Teodorico L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110 1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,954
;      FILING DATE:
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,821
;      REFERENCE/DOCKET NUMBER:  8873
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814 2974
;      TELEFAX:  (510) 814 2977
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-127-954-61

  Query Match             91.6%;  Score 1234;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches  180;  Conservative    0;  Mismatches    11;  Indels    0;  Gaps    0;

Qy       1 TAGTGGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TAGTGGGACAGACACGCAGT 97


RESULT 10
US-08-127-954-62
; Sequence 62, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;    APPLICANT:  Apple, Raymond J.
;    APPLICANT:  Bugawan, Teodorico L.
;    APPLICANT:  Erlich, Henry A.
;    TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;    TITLE OF INVENTION:  Locus DNA Typing
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110 1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/127,954
;       FILING DATE:
;       CLASSIFICATION:  436
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petry, Douglas A.
;       REGISTRATION NUMBER:  35,321
;       REFERENCE/DOCKET NUMBER:  8873
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 814-2974
;       TELEFAX:  (510) 814-2977
;   INFORMATION FOR SEQ ID NO:  62:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  270 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-127-954-62

  Query Match             91.6%;  Score 17.4;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 11
US-08-127-954-63
; Sequence 63, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;     APPLICANT:  Apple, Raymond J.
;     APPLICANT:  Bugawan, Teodorica L.
;     APPLICANT:  Erlich, Henry A.
;     TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;     TITLE OF INVENTION:  Locus DNA Typing
;     NUMBER OF SEQUENCES:  173
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Hoffmann-La Roche Inc.
;       STREET:  340 Kingsland Street
;       CITY:  Nutley
;       STATE:  New Jersey
;       COUNTRY:  U.S.A.
;       ZIP:  07110-1199
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/127,954
;       FILING DATE:
;       CLASSIFICATION:  436
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petry, Douglas A.
;       REGISTRATION NUMBER:  35,321
;       REFERENCE/DOCKET NUMBER:  8873
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 814-2974
;       TELEFAX:  (510) 814-2977
;   INFORMATION FOR SEQ ID NO:  63:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  270 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-127-954-63

  Query Match             91.6%;  Score 17.4;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 12
US-08-127-954-64
; Sequence 64, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;     APPLICANT:  Apple, Raymond J.
;     APPLICANT:  Bugawan, Teodorica L.
;     APPLICANT:  Erlich, Henry A.
;     TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;     TITLE OF INVENTION:  Locus DNA Typing
;     NUMBER OF SEQUENCES:  173
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Hoffmann-La Roche Inc.
;       STREET:  340 Kingsland Street
;       CITY:  Nutley
;       STATE:  New Jersey
;       COUNTRY:  U.S.A.
;       ZIP:  07110-1199
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/127,954
;       FILING DATE:
;       CLASSIFICATION:  436
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petry, Douglas A.
;       REGISTRATION NUMBER:  35,321
;       REFERENCE/DOCKET NUMBER:  8873
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 814-2974
;       TELEFAX:  (510) 814-2977
;   INFORMATION FOR SEQ ID NO:  64:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  270 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-127-954-64

  Query Match             91.6%;  Score 17.4;  DB 1;  Length 270;
  Best Local Similarity   94.7%;  Pred. No. 2.6;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db      78 TACGTGGACGACACGCAGT 96


RESULT 13
US-08-127-954-65
; Sequence 65, Application US/08127954
; Patent No. 5451512
;  GENERAL INFORMATION:
;     APPLICANT:  Apple, Raymond J.
;     APPLICANT:  Bugawan, Teodorica L.
;     APPLICANT:  Erlich, Henry A.
;     TITLE OF INVENTION:  Methods and Reagents for HLA Class I A
;     TITLE OF INVENTION:  Locus DNA Typing
```

; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,954
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,421
; REFERENCE/DOCKET NUMBER: 9873
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-127-954-65

Query Match 91.6%; Score 17.4; DB 1; Length 270;
Best Local Similarity 94.7%; Pred. No. 2.6;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACCTGGACAACACGCAGT 19
|||||||||| |||||||||
Db 78 TACCTGGACGACACGCAGT 96

RESULT 14
US-08-127-954-66
; Sequence 66, Application US/08127954
; Patent No. 5451512
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; TITLE OF INVENTION: Methods and Reagents for HLA Class I A
; TITLE OF INVENTION: Locus DNA Typing
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,954
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,421
; REFERENCE/DOCKET NUMBER: 9873
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-127-954-66

Query Match 91.6%; Score 17.4; DB 1; Length 270;
Best Local Similarity 94.7%; Pred. No. 2.6;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACCTGGACAACACGCAGT 19
|||||||||| |||||||||
Db 78 TACCTGGACGACACGCAGT 96

RESULT 15
US-08-127-954-67
; Sequence 67, Application US/08127954
; Patent No. 5451512
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; TITLE OF INVENTION: Methods and Reagents for HLA Class I A
; TITLE OF INVENTION: Locus DNA Typing
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,954
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,421
; REFERENCE/DOCKET NUMBER: 9873
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-127-954-67

Query Match 91.6%; Score 17.4; DB 1; Length 270;
Best Local Similarity 94.7%; Pred. No. 2.6;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACCTGGACAACACGCAGT 19
|||||||||| |||||||||
Db 78 TACCTGGACGACACGCAGT 96

Search completed: April 15, 2003, 01:45:41
Job time : 90 secs

; PRIOR APPLICATION NUMBER: US 60/244,697
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17524
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB024057.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL 0.87
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL 2.1
; OTHER INFORMATION: EST_HUMAN hit: AB039120.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: AF226990.2, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P17693, EVALUE 1.00e-49
US-09-960-352-17524

Query Match 91.6%; Score 17.4; DB 10; Length 270;
Best Local Similarity 94.7%; Pred. No. 3.9;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||||||| |||||||||
Db 193 TACGTGGACGACACGCAGT 175

RESULT 2
US-09-960-352-5480
; Sequence 5480, Application US/09960352
; Patent No. US20020137149A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5480
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 24-LIB188-011-Q1-E1-F7
US-09-960-352-5480

Query Match 91.6%; Score 17.4; DB 10; Length 282;
Best Local Similarity 94.7%; Pred. No. 3.9;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||||||| |||||||||
Db 268 TACGTGGACGACACGCAGT 250

RESULT 3
US-09-960-352-2832
; Sequence 2832, Application US/09960352
; Patent No. US20020137149A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2832
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 13-LIB188-005-Q1-E1-D9
US-09-960-352-2832

Query Match 91.6%; Score 17.4; DB 10; Length 306;
Best Local Similarity 94.7%; Pred. No. 3.9;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||||||| |||||||||
Db 99 TACGTGGACGACACGCAGT 97

RESULT 4
US-09-960-352-13958
; Sequence 13958, Application US/09960352
; Patent No. US20020137149A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 13958
; LENGTH: 308
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (8)
; OTHER INFORMATION: unsure at all n locations
; US-09-960-352-13958

Query Match 91.6%; Score 17.4; DB 10; Length 308;
Best Local Similarity 94.7%; Pred. No. 3.9;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||||||| |||||||||
Db 41 TACGTGGACGACACGCAGT 59

RESULT 5
US-09-920-455-205
; Sequence 205, Application US/09920455
; Patent No. US20020168647A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF HEAD AND NECK CANCER

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OM nucleic - nucleic search, using sw model

Run on:          April 15, 2003, 00:56:07 ; Search time 77 Seconds
                                           (without alignments)
                                           216.444 Million cell updates/sec

Title:           US-09-856-662-3
Perfect score:   19
Sequence:        1 tacgtggacaacacgcagt 19

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        [illegible] seqs, [illegible] residues

Total number of hits satisfying chosen parameters:      1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
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                 2:  [illegible]_pubpna/PCT_NEW_PUB.seq:*
                 3:  [illegible]_pubpna/US06_NEW_PUB.seq:*
                 4:  [illegible]_pubpna/US06_PUBCOMB.seq:*
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                 10: [illegible]_pubpna/US09_PUBCOMB.seq:*
                 11: [illegible]_pubpna/US10_NEW_PUB.seq:*
                 12: [illegible]_pubpna/US10_PUBCOMB.seq:*
                 13: [illegible]_pubpna/US60_NEW_PUB.seq:*
                 14: [illegible]_pubpna/US60_PUBCOMB.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17.4	91.6	270	10	US-09-864-761-17524	Sequence 17524, A
c	2	17.4	91.6	282	10	US-09-960-352-5182	Sequence 5182, Ap
	3	17.4	91.6	306	10	US-09-960-352-2832	Sequence 2832, Ap
	4	17.4	91.6	308	10	US-09-960-352-13958	Sequence 13958, A
	5	17.4	91.6	405	9	US-09-920-455-205	Sequence 205, App
	6	17.4	91.6	422	10	US-09-960-352-9792	Sequence 9792, Ap
c	7	17.4	91.6	428	10	US-09-960-352-2127	Sequence 2127, Ap
c	8	17.4	91.6	439	10	US-09-864-761-739	Sequence 739, App
	9	17.4	91.6	468	9	US-09-854-133-133	Sequence 133, App
	10	17.4	91.6	468	10	US-09-778-072-133	Sequence 133, App
	11	17.4	91.6	524	10	US-09-815-343-771	Sequence 771, App
	12	17.4	91.6	1048	9	US-10-073-800-1	Sequence 1, Appl
	13	17.4	91.6	1082	10	US-09-969-347-218	Sequence 218, App
	14	17.4	91.6	1155	12	US-10-044-090-562	Sequence 562, App
	15	17.4	91.6	1377	12	US-10-044-090-563	Sequence 563, App
	16	17.4	91.6	1466	12	US-10-044-090-564	Sequence 564, App
	17	17.4	91.6	1526	12	US-10-044-090-561	Sequence 561, App
	18	16.4	86.3	426	10	US-09-960-352-2995	Sequence 2995, Ap
	19	15.8	83.2	292	10	US-09-960-352-12574	Sequence 12574, A
	20	15.8	83.2	400	10	US-09-854-124-16	Sequence 16, Appl
c	21	15.8	83.2	309	10	US-09-960-352-9703	Sequence 9703, Ap
c	22	15.8	83.2	311	10	US-09-864-761-32045	Sequence 32045, A
c	23	15.8	83.2	455	10	US-09-864-761-15533	Sequence 15533, A
	24	15.8	83.2	510	9	US-09-920-455-184	Sequence 184, App
	25	15.8	83.2	675	12	US-10-044-090-522	Sequence 522, App
	26	15.8	83.2	720	9	US-10-015-535-33	Sequence 33, Appl
	27	15.8	83.2	832	9	US-10-015-535-31	Sequence 31, Appl
	28	15.8	83.2	1091	9	US-10-015-535-35	Sequence 35, Appl
	29	15.8	83.2	1271	10	US-09-969-708-38	Sequence 38, App
	30	15.8	83.2	1571	12	US-10-044-090-576	Sequence 576, App
	31	15.8	83.2	1632	9	US-10-015-535-21	Sequence 21, Appl
	32	15.8	83.2	1640	9	US-10-015-535-23	Sequence 23, Appl
	33	15.8	83.2	1640	9	US-10-015-535-25	Sequence 25, Appl
	34	15.8	83.2	1640	9	US-10-015-535-27	Sequence 27, Appl
	35	14.8	77.9	292	10	US-09-960-352-11912	Sequence 11912, A
	36	14.4	75.8	1164	9	US-09-738-626-1590	Sequence 1590, Ap
	37	14.4	75.8	2405	10	US-09-764-887-484	Sequence 484, App
	38	14.4	75.8	2736	9	US-09-908-871A-56	Sequence 56, Appl
	39	14.4	75.8	5216	10	US-09-880-107-1538	Sequence 1538, Ap
c	40	14.2	74.7	351	10	US-09-960-352-4606	Sequence 4606, Ap
	41	14.2	74.7	356	10	US-09-960-352-4596	Sequence 4596, Ap
c	42	14.2	74.7	379	10	US-09-960-352-828	Sequence 828, App
	43	14.2	74.7	816	10	US-09-925-301-589	Sequence 589, App
c	44	14.2	74.7	906	9	US-09-954-531-128	Sequence 128, App
c	45	14.2	74.7	975	9	US-09-738-626-1738	Sequence 1738, Ap

ALIGNMENTS

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RESULT 1
US-09-864-761-17524/c
; Sequence 17524, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT: Rank, David R.
;  APPLICANT: Hanzel, David K.
;  APPLICANT: Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
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;  FILE REFERENCE: 21(121/C3
;  CURRENT APPLICATION NUMBER:  US/09/920,455
;  CURRENT FILING DATE:  2001-08-01
;  NUMBER OF SEQ ID NOS: 275
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205
;   LENGTH: 405
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 378, 379, 398
;   OTHER INFORMATION: n = A,T,C or G
US-09-920-455-205

  Query Match             91.6%;  Score 17.4;  DB 9;  Length 405;
  Best Local Similarity   94.7%;  Pred. No. 4;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||| ||||||||||
Db     157 TACGTGGACGACACGCAGT 175


RESULT 6
US-09-960-352-9792
; Sequence 9792, Application US/09960352
; Patent No. US20020147139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nongbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37.21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9792
;   LENGTH: 422
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 12-LIB1078-011-Q1-E1-C5
US-09-960-352-9792

  Query Match             91.6%;  Score 17.4;  DB 10;  Length 422;
  Best Local Similarity   94.7%;  Pred. No. 4;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||| ||||||||||
Db     149 TACGTGGACGACACGCAGT 167


RESULT 7
US-09-960-352-2127
; Sequence 2127, Application US/09960352
; Patent No. US20020147139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nongbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37.21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2127
;   LENGTH: 429
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 10-LIB188-011-Q1-E1-C5
US-09-960-352-2127

  Query Match             91.6%;  Score 17.4;  DB 10;  Length 428;
  Best Local Similarity   94.7%;  Pred. No. 4;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||| ||||||||||
Db     268 TACGTGGACGACACGCAGT 250


RESULT 8
US-09-864-761-739
; Sequence 739, Application US/09864761
; Patent No. US20020034763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER:  US/09/864,761
;  CURRENT FILING DATE:  2001-05-24
;  PRIOR APPLICATION NUMBER: US 60/166,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 0024263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 09/236,459
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/771,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Aeomomx Sequence Listing Engine vers. 1.1
; SEQ ID NO 739
;   LENGTH: 439
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AB023057.1
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN COLO, SIGNAL = 3.1
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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL 2.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL 1.1
; OTHER INFORMATION: EXPRESSED IN RI474, SIGNAL 0.97
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL 1.1
US-09-864-261-709

Query Match 91.6%; Score 17.4; DB 10; Length 439;
Best Local Similarity 94.7%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||| ||| |||||||||
Db 435 TACGTGGACGACACGCAGT 417

RESULT 9
US-09-854-133-133
; Sequence 133, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-854-133-133

Query Match 91.6%; Score 17.4; DB 9; Length 468;
Best Local Similarity 94.7%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
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Db 153 TACGTGGACGACACGCAGT 171

RESULT 10
US-09-738-973-133
; Sequence 133, Application US/09738973
; Patent No. US20020110564A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Alpate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT [illegible] DATE: 2000-12-14

; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-738-973-133

Query Match 91.6%; Score 17.4; DB 10; Length 468;
Best Local Similarity 94.7%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||||||| |||||||||
Db 153 TACGTGGACGACACGCAGT 171

RESULT 11
US-09-815-343-771
; Sequence 771, Application US/09815343
; Patent No. US20010055596A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine
; APPLICANT: Xu, Jianchun
; APPLICANT: Kind, Gordon E.
; TITLE OF INVENTION: [illegible] AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.504
; CURRENT APPLICATION NUMBER: US/09/815,343
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(524)
; OTHER INFORMATION: n = A,T,C or G
US-09-815-343-771

Query Match 91.6%; Score 17.4; DB 10; Length 524;
Best Local Similarity 94.7%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TACGTGGACAACACGCAGT 19
||||||||| |||||||||
Db 158 TACGTGGACGACACGCAGT 176

RESULT 12
US-10-073-800-4
; Sequence 4, Application US/10073800
; Publication No. US20040005581A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES
; FILE REFERENCE: 02/23339
; CURRENT APPLICATION NUMBER: US/10/073,800
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-073-800-4

Query Match 91.6%; Score 17.4; DB 9; Length 1048;
Best Local Similarity 94.7%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 TACGTGGACAACACGCAGT 19
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Db     424 TACGTGGACGACACGCAGT 442


RESULT 13
US-09-969-347-218
; Sequence 218, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-69
;  CURRENT APPLICATION NUMBER: US/09/969,347
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US/60/237,598
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: US/60/237,604
;  PRIOR FILING DATE: 2000-10-03
;  NUMBER OF SEQ ID NOS: 318
;  SOFTWARE: Patentin version 3.0
; SEQ ID NO 218
;  LENGTH: 1082
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-969-347-218

  Query Match             91.6%;  Score 17.4;  DB 10;  Length 1082;
  Best Local Similarity   94.7%;  Pred. No. 4.2;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
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Db     175 TACGTGGACGACACGCAGT 193


RESULT 14
US-10-044-090-562
; Sequence 562, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
;  APPLICANT: Olga Bandman
;  TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
;  FILE REFERENCE: PA-0028 US
;  CURRENT APPLICATION NUMBER: US/10/044,090
;  CURRENT FILING DATE:  2002-01-09
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: PERL Program
; SEQ ID NO 562
;  LENGTH: 1155
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No: US20020137081A1 1383423.1
;  NAME/KEY: unsure
;  LOCATION: 344, 394
;  OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-562

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  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
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Db     160 TACGTGGACGACACGCAGT 178


RESULT 15
US-10-044-090-563
; Sequence 563, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
;  APPLICANT: Olga Bandman
;  TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
;  FILE REFERENCE: PA-0028 US
;  CURRENT APPLICATION NUMBER: US/10/044,090
;  CURRENT FILING DATE:  2002-01-09
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: PERL Program
; SEQ ID NO 563
;  LENGTH: 1377
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No: US20020137081A1 1817377CB1
;  NAME/KEY: unsure
;  LOCATION: 1350
;  OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-563

  Query Match             91.6%;  Score 17.4;  DB 12;  Length 1377;
  Best Local Similarity   94.7%;  Pred. No. 4.2;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||| |||||||||
Db     240 TACGTGGACGACACGCAGT 258


Search completed: April 15, 2003, 01:17:12
Job time : 78 secs
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Site Copy

GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 08:27:37 ; Search time 1091 Seconds
(without alignments)
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Title: US-09-856-662-3
Perfect score: 19
Sequence: 1 tacgtggacaacacgcaqt 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	100.0	349	4	BTMHC2	X97645 B.taurus MH
2	19	100.0	699	4	AF[illegible]625	AF[illegible]625 Bos taurus
3	19	100.0	942	9	MMU55465	U55465 Macaca mula
4	19	100.0	961	9	MMU55466	U55466 Macaca mula
5	19	100.0	1056	9	PTU10538	U10538 Pan troglod
6	19	100.0	1074	9	ARU59649	U59649 Ateles belz
7	19	100.0	1074	9	PTU10541	U10541 Pan troglod
8	19	100.0	1074	9	SFU59635	U59635 Saguinus fu
9	19	100.0	1092	9	AF179638	AF179638 Pan trogl
10	19	100.0	1092	9	AF179639	AF179639 Pan trogl
11	19	100.0	1098	9	AF168404	AF168404 Pan trogl
12	19	100.0	1098	9	AF168405	AF168405 Pan trogl
13	19	100.0	1098	9	HSU55825	U55825 Human MHC c
14	19	100.0	1269	9	CHPMHC02A	L39094 Pan paniscu
15	19	100.0	1429	9	MMU55967	U55967 Macaca mula
16	19	100.0	3534	4	CATMH1PS	M27192 Cat MHC cla
17	19	100.0	4409	10	MMU21906	U21906 Mus musculu
18	18	94.7	262	10	PELEM109G1	AF079430 Peromysc
19	18	94.7	262	10	PELEM47G1	AF079432 Peromysc
20	18	94.7	262	10	PELEM157G1	AF079434 Peromysc
21	18	94.7	262	10	PELEM412G1	AF079436 Peromysc
22	18	94.7	262	10	PELEM43G1	AF079438 Peromysc
23	18	94.7	262	10	PELEM419G1	AF079440 Peromysc
24	18	94.7	262	10	PELEM416G1	AF079442 Peromysc
25	18	94.7	5644	10	AF006618	AF006618 Peromysc
26	17.4	91.6	111	10	MUSMB37I01	M34072 Mus musculu
27	17.4	91.6	190	4	AF074481	AF074481 Sus scrof
28	17.4	91.6	194	9	HLACW402	U31473 Human class
29	17.4	91.6	196	9	HSHLAA0X2	X83082 H.sapiens H
30	17.4	91.6	196	9	HSHLAA2X2	X83004 H.sapiens H
31	17.4	91.6	203	10	RN0243582	AI243582 Rattus no
32	17.4	91.6	212	9	AF100667	AF100667 Homo sapi
33	17.4	91.6	228	9	HSC402N1	U60422 Human MHC c
34	17.4	91.6	229	9	HSC701N1	U61273 Human MHC c
35	17.4	91.6	237	9	HSC2022N1	U60215 Human MHC c
36	17.4	91.6	241	9	CHPMHCLA	M95737 Pan troglod
37	17.4	91.6	241	9	GORMHCLA	M95736 Gorilla gor
38	17.4	91.6	241	9	GGMHCG2	X65745 G.gorilla D
39	17.4	91.6	241	9	HSHLAGAG	X60988 H.sapiens g
40	17.4	91.6	241	9	HSHLAATE2	Y12470 H.sapiens H
41	17.4	91.6	241	9	HUMHLAGA	L27836 Human MHC c
42	17.4	91.6	241	9	PPH33289	U33289 Pan paniscu
43	17.4	91.6	241	9	PPU33292	U33292 Pongo pygma
44	17.4	91.6	241	9	PPU33294	U33294 Pongo pygma
45	17.4	91.6	241	9	PTMHCG2	X65744 P.troglodyt

ALIGNMENTS

RESULT 1
BTMHC2
LOCUS PTMHC2 349 bp DNA linear MAM 02-DEC 1996
DEFINITION B.taurus MHC class 1 gene, exon 2 (and joined CDS).
ACCESSION X97645
VERSION X97645.1 GI:1121697
KEYWORDS MHC class 1 gene.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 349)
AUTHORS Russell,G.C., Oliver,R.A. and Sawhney,S.M.
TITLE Cloning, transfection, and DNA sequence of a second gene from the

```
            BoLA A11 haplotype
  JOURNAL   Immunogenetics 44 (4), 315-318 (1996)
  MEDLINE   96337924
   PUBMED   8753865
REFERENCE   2  (bases 1 to 349)
  AUTHORS   Russell,G.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-1996) G.C. Russell, Roslin Institute, Roslin,
            Midlothian, EH25 9PS, UK
FEATURES             Location/Qualifiers
     source          1..349
                     /organism="Bos taurus"
                     /isolate="animal 10769"
                     /sub_species="Holstein friesian"
                     /db_xref="taxon:9913"
                     /chromosome="23"
                     /map="q21-qter Map Units (mu)"
                     /clone="pBoLA-4"
                     /haplotype="BoLA A11 /A11"
                     /cell_type="peripheral blood monocytes"
                     /clone_lib="EMBL clone 4.2"
                     /dev_stage="adult"
                     /germline
     gene            2..271
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     mRNA            join(<2..271,X97646.1:50..325,X97647.1:67..342,
                     X97647.1:459..563,X97648.1:46..78,X97649.1:37..84,
                     X97649.1:247..>442)
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     CDS             join(2..271,X97646.1:50..325,X97647.1:67..342,
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                     X97649.1:247..251)
                     /gene="MHC class I"
                     /codon_start=3
                     /label=mhc_cds
                     /product="MHC class I heavy chain"
                     /protein_id="CAA66250.1"
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                     /db_xref="SPTREMBL:Q30287"
                     /translation="SHSLRYFLTPVSRPDLGPPRYLEVGYVDDNTQFVRFDSDARNPRM
                     EPRARWVEQEGPEYWDQNTRNSKGAAQTFRVDLNTLRGYYNQSEAGSHTIQAMYGCDV
                     GPDGRFLRGYRQDAYDGRDYIALNEDLRSWTAADTAAQITKRKWEEAGAAEGERNYLE
                     GTCVEWLRRYLENGKDALLRADPPKAHVTHHPISDREVTLRCWALGFYPEEISLTWQR
                     EGEDQTQDMELVETRPSGDGSFQKWAAIVVPSGEEQRYTCRVQHKGLQEPITLIWEPP
                     QPSVPIMGIVVGLVLLVAVVAGAVIWRKKCSGEKGQTYTQAASSDSDQGSDVSRTVP
                     KV"
     exon            <2..271
                     /gene="MHC class I"
                     /label=ex2
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
                |||||||||||||||||||
Db         79 TACGTGGACAACACGCAGT 97

RESULT 2
AB008625
LOCUS       AB008625                 699 bp    DNA     linear   MAM 14-APR-2000
DEFINITION  Bos taurus gene for MHC class I heavy chain, partial cds, clone
            no.26-12q.
ACCESSION   AB008625
VERSION     AB008625.1  GI:2864767
KEYWORDS    MHC class I heavy chain.
SOURCE      Bos taurus (variety:Holstein, isolate:no.26) peripheral blood
            monocytes DNA, clone:no.26-12q.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 699)
  AUTHORS   Urakawa,T., Kodama,M., Morita,M. and Ikeda,H.
  TITLE     Diversity of Bovine MHC class I related sequences
  JOURNAL   Published Only in DataBase (1998)
REFERENCE   2  (bases 1 to 699)
  AUTHORS   Urakawa,T., Kodama,M., Morita,M. and Ikeda,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1997) Toyohiko Urakawa, STAFF Institute, 2nd
            Division; 446-1 Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305, Japan
            (E-mail:urakawa@gene.staff.or.jp, Tel:+81-298-38-7757,
            Fax:+81-298-38-7880)
FEATURES             Location/Qualifiers
     source          1..699
                     /organism="Bos taurus"
                     /variety="Holstein"
                     /isolate="no.26"
                     /db_xref="taxon:9913"
                     /clone="no.26-12q"
                     /cell_type="monocytes"
                     /tissue_type="peripheral blood"
                     /note="Bovine MHC class I haplotype (A10/ ): PCR amplified
                     clone"
     CDS             join(<1..256,455..>699)
                     /function="antigen presentation"
                     /standard_name="MHC class I related gene"
                     /note="cell surface antigen; cell surface glycoprotein;
                     BoLA class I gene; integral membrane protein; major
                     histocompatibility complex
                     particial alpha 1 and 2 domains"
                     /codon_start=1
                     /product="MHC class I heavy chain"
                     /protein_id="BAA24754.1"
                     /db_xref="GI:2864768"
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                     RWVEQEGPEYWDQNTRNSKGAAQTFRVDLNTLRGYYNQSEAGSHTIQAMYGCDVGPDG
                     RFLRGYRQDAYDGRDYIALNEDLRSWIAADTAAQITKRKWEEAGAAEGERNYLEGTCV
                     EWLRRYL"
     exon            1..256
                     /number=2
     intron          257..454
                     /number=2
     exon            455..699
                     /number=3
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACGTGGACAACACGCAGT 19
                |||||||||||||||||||
Db         64 TACGTGGACAACACGCAGT 82

RESULT 3
MMU55065
LOCUS       MMU55065                 932 bp    mRNA    linear   PRI 15-JAN-1997
DEFINITION  Macaca mulatta MHC class I HLA-C ortholog (Mamu-C*01) pseudogene
            mRNA, splice variant, partial cds.
ACCESSION   U55065
VERSION     U55065.1  GI:1322301
KEYWORDS    .
SOURCE      Macaca mulatta.
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 932)
  AUTHORS   Boyson,J.E., Iwanaga,K.K., Golos,T.G. and Watkins,D.I.
```

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  TITLE     Identification of the rhesus monkey HLA-G ortholog. Mamu-G is a
            pseudogene
  JOURNAL   J. Immunol. 157 (12), 5428-5437 (1996)
  MEDLINE   97113331
   PUBMED   8955191
REFERENCE   2  (bases 1 to 932)
  AUTHORS   Boyson,J.E., Iwanaga,K.K., Golos,T.G. and Watkins,D.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-1996) Jonathan E. Boyson, Pathology, Wisconsin
            Regional Primate Research Center, 1220 Capitol Court, Madison, WI
            53715, USA
FEATURES             Location/Qualifiers
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BASE COUNT      194 a    246 c    326 g    166 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 14;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGGCAGT 19
           ||||||||||||||||||||
Db     124 TACGTGGACAACACGGCAGT 142


RESULT 4
MMU55066
LOCUS       MMU55066                 961 bp    mRNA    linear   FRI 15-JAN 1997
DEFINITION  Macaca mulatta MHC class I HLA-G ortholog (Mamu-G*01) pseudogene
            mRNA, splice variant, partial sequence.
ACCESSION   U55066
VERSION     U55066.1  GI:1322302
KEYWORDS    .
SOURCE      Macaca mulatta.
  ORGANISM  Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 961)
  AUTHORS   Boyson,J.E., Iwanaga,K.K., Golos,T.G. and Watkins,D.I.
  TITLE     Identification of the rhesus monkey HLA-G ortholog. Mamu-G is a
            pseudogene
  JOURNAL   J. Immunol. 157 (12), 5428-5437 (1996)
  MEDLINE   97113331
   PUBMED   8955191
REFERENCE   2  (bases 1 to 961)
  AUTHORS   Boyson,J.E., Iwanaga,K.K., Golos,T.G. and Watkins,D.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-1996) Jonathan E. Boyson, Pathology, Wisconsin
            Regional Primate Research Center, 1220 Capitol Court, Madison, WI
            53715, USA
FEATURES             Location/Qualifiers
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                     /clone="1571-6"
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  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGGCAGT 19
           ||||||||||||||||||||
Db     124 TACGTGGACAACACGGCAGT 142


RESULT 5
PTU10538
LOCUS       PTU10538                 1056 bp    mRNA    linear   FRI 22-FEB-1996
DEFINITION  Pan troglodytes clone PatrA08 MHC class I A mRNA, partial cds.
ACCESSION   U10538
VERSION     U10538.1  GI:506667
KEYWORDS    .
SOURCE      Pan troglodytes.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1056)
  AUTHORS   McAdam,S.N., Boyson,J.E., Liu,X., Garber,T.L., Hughes,A.L.,
            Bontrop,R.E. and Watkins,D.I.
  TITLE     Chimpanzee MHC class I A locus alleles are related to only one of
            the six families of human A locus alleles
  JOURNAL   J. Immunol. 154 (12), 6421-6429 (1995)
  MEDLINE   95279794
   PUBMED   7759878
REFERENCE   2  (bases 1 to 1056)
  AUTHORS   Boyson,J.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1994) Jonathan E. Boyson, Wisconsin Regional
            Primate Research Center, 1220 Capitol Court, Madison, WI 53715, USA
FEATURES             Location/Qualifiers
     source          1..1056
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                     /db_xref="taxon:9598"
                     /clone="PatrA08"
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                     RKWEAAHAAEQFRAYLEGTCVEWLRRYLENGKETLQRTDPPKTHMTHHPISDHEATLR
                     CWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCH
                     VQHEGLPKPLTLRWEPSSQPTIPIVGIIAGLVLFGAVVTGAVVAAVMWRRKSSDRKGG
                     SYSQAASSDSAQGSDVSL"
BASE COUNT      209 a    321 c    354 g    172 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGGCAGT 19
           ||||||||||||||||||||
Db     127 TACGTGGACAACACGGCAGT 145


RESULT 6
ABU59649
LOCUS       ABU59649                 1074 bp    mRNA    linear   FRI 23-JAN-1998
DEFINITION  Ateles belzebuth MHC class I (Atbe-G*02) mRNA, partial cds.
ACCESSION   U59649
VERSION     U59649.1  GI:1389910
KEYWORDS    .
SOURCE      Ateles belzebuth.
  ORGANISM  Ateles belzebuth
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae;
            Ateles.
REFERENCE   1  (bases 1 to 1074)
  AUTHORS   Cadavid,L.F., Shufflebotham,C., Ruiz,F.J., Yeager,M., Hughes,A.L.
            and Watkins,D.I.
  TITLE     Evolutionary instability of the major histocompatibility complex
            class I loci in New World primates
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14536-14541 (1997)
  MEDLINE   98070787
   PUBMED   9405648
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REFERENCE   2  (bases 1 to 1074)
  AUTHORS   Cadavid,L.F., Shuttlebotham,C., Ruiz,F.J., Yeager,M., Hughes,A.L.
            and Watkins,D.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-1996) Wisconsin Regional Primate Research Center,
            University of Wisconsin-Madison, 1220 Capitol Court, Madison, WI
            53715, USA
FEATURES             Location/Qualifiers
     source          1..1074
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     gene            1..1074
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                     /translation="VLLLLSEALALTETWASSYSMKYFFTALSRPGRGEPRFISVGYV
                     DNTQFLWFDSDAATPRAEPRAPWAEQEGEEYWDWNTRFCKTNAQTYRENLRTLRGYYN
                     QSEEGSHTIQSLHGCDLGPDGRLLRGYHQFAYDGKDYIALNEDLRSWTAADVVAQITQ
                     RKWEAANEAEQNKAYLEGRCVEGLRKYLENGKETLQRTDPPKTHMTHHPISDHEATLR
                     CWALGFYPAEITLTWQRDGEDQTQDMELVETRPAGDGTFQKWAAVVVPSGEEQRYTCH
                     VQHEGLPEPLTLRWEPPSQPTIPIVGIVAGLAVLAAIVTGAVVAAVMWRKKSSDRGG
                     SYSQAASSDSAQGSDVSLTACKV"
BASE COUNT       224 a     315 c     343 g     192 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 9;  Length 1074;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||||||||||||
Db     127 TACGTGGACAACACGGCAGT 145


RESULT 7
PTU10541
LOCUS       PTU10541                1074 bp    mRNA    linear   PRI 22-FEB-1996
DEFINITION  Pan troglodytes clone PatrA10 MHC class I A mRNA, partial cds.
ACCESSION   U10541
VERSION     U10541.1  GI:506673
KEYWORDS    .
SOURCE      Pan troglodytes.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1074)
  AUTHORS   McAdam,S.N., Boyson,J.E., Liu,X., Garber,T.L., Hughes,A.L.,
            Bontrop,R.E. and Watkins,D.I.
  TITLE     Chimpanzee MHC class I A locus alleles are related to only one of
            the six families of human A locus alleles
  JOURNAL   J. Immunol. 154 (12), 6421-6429 (1995)
  MEDLINE   95279794
   PUBMED   7759878
REFERENCE   2  (bases 1 to 1074)
  AUTHORS   Boyson,J.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1994) Jonathan E. Boyson, Wisconsin Regional
            Primate Research Center, 1220 Capitol Court, Madison, WI 53715, USA
FEATURES             Location/Qualifiers
     source          1..1074
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PatrA10"
     CDS             <1..1074
                     /codon_start=1
                     /product="MHC class I A"
                     /protein_id="AAA88856.1"
                     /db_xref="GI:506674"
                     /translation="LVLLLSGALALTETWAGSHSMRYFSTSVSRPGRGEPRFIAVGYV
                     DNTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDQETRNMKAHAQTYRANLGTLRGYYN
                     QSEDGSHTIQLMFGCDVGSDGRFLRGYRQFAYDGKDYIALNEDLRSWTAADMAAQITQ
                     RKWEAAHAAEQWKAYLEGRCVEGLRKYLENGKETLQRTDPPKTHMTHHPISDREATLR
                     CWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCH
                     VQHEGLEKPLTLRWEPSSQSTIPIVGIVAGLAVLAVIVIGAVVAAVMWRRKSSDRKGG
                     SYSQAASSDSAQGSDVSLTACKV"
BASE COUNT       216 a     321 c     358 g     179 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 9;  Length 1074;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||||||||||||
Db     127 TACGTGGACAACACGCAGT 145


RESULT 8
SFU59645
LOCUS       SFU59645                1074 bp    mRNA    linear   PRI 22-JAN-1998
DEFINITION  Saguinus fuscicollis MHC class I (Safu-G*02) mRNA, partial cds.
ACCESSION   U59645
VERSION     U59645.1  GI:1089950
KEYWORDS    .
SOURCE      Saguinus fuscicollis.
  ORGANISM  Saguinus fuscicollis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
            Saguinus.
REFERENCE   1  (bases 1 to 1074)
  AUTHORS   Cadavid,L.F., Shuttlebotham,C., Ruiz,F.J., Yeager,M., Bontrop,R.E.
            and Watkins,D.I.
  TITLE     Evolutionary instability of the major histocompatibility complex
            class I loci in New World primates
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14540-14541 (1997)
  MEDLINE   98070787
   PUBMED   9405648
REFERENCE   2  (bases 1 to 1074)
  AUTHORS   Cadavid,L.F., Shuttlebotham,C., Ruiz,F.J., Yeager,M., Hughes,A.L.
            and Watkins,D.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-1996) Wisconsin Regional Primate Research Center,
            University of Wisconsin-Madison, 1220 Capitol Court, Madison, WI
            53715, USA
FEATURES             Location/Qualifiers
     source          1..1074
                     /organism="Saguinus fuscicollis"
                     /db_xref="taxon:9487"
     gene            1..1074
                     /gene="MHC class I Safu-G"
     CDS             <1..1074
                     /gene="MHC class I Safu-G"
                     /note="Allele: 02"
                     /codon_start=1
                     /product="MHC class I Safu-G*02"
                     /protein_id="AAB97496.1"
                     /db_xref="GI:1389995"
                     /translation="LVLLLSGALALTETWAGSHSMRYFSTSVSRPGRGEPRFIAVGYV
                     DNTQFVRFDSDAASPRMEPRAPWVEQEGPEYWEEQTRKAKAHAQTFRVNLQTLRGYYN
                     QSEAGSHTIQWMSGCDLGPDGRLLRGYLQDAYDGKDYIALNEDLRSWTAADVAAQITQ
                     RKWEAANVAEQWRAYLEGECVEGLRRYLENGKETLQRADPPKTHVTHHPISDHEATLR
                     CWALGFYPAEITLTWQRDGEDQTQDMELVETRPAGDGTFQKWAAVVVLSGQEHRYTCH
                     VQHEGLPKPLTLRWEPSQPTIPIMGIVAGLAVLAIIAIGAVVIGAVVAAVMCRRKSSGKKGG
                     SYSQAARSDSAQGSDVSLIACKV"
BASE COUNT       222 a     322 c     356 g     174 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 9;  Length 1074;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||||||||||||||
Db     127 TACGTGGACAACACGCAGT 145


RESULT 9
AF179648
LOCUS       AF179648                1092 bp    mRNA    linear   PRI 19-JUN-2000
DEFINITION  Pan troglodytes MHC class I antigen (Patr A) mRNA, Patr A*0802
            allele, partial cds.
ACCESSION   AF179648
VERSION     AF179648.1  GI:8571964
KEYWORDS    .
SOURCE      Pan troglodytes.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1092)
  AUTHORS   Adams,E.J., Cooper,S., Thomson,G. and Parham,P.
  TITLE     Common chimpanzees have greater diversity than humans at two of the
            three highly polymorphic MHC class I genes
  JOURNAL   Immunogenetics 51 (6), 410-424 (2000)
  MEDLINE   20322476
   PUBMED   10866107
REFERENCE   2  (bases 1 to 1092)
  AUTHORS   Adams,E.J., Cooper,S., Thomson,G. and Parham,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (24 AUG 1999) Structural Biology (Stanford)/Integrative
            Biology (UC Berkeley), Stanford University/UC Berkeley, Campus
            Drive West, Stanford, CA 94305, USA
FEATURES             Location/Qualifiers
     source          1..1092
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /cell_type="BLCL"
     gene            <1..1092
                     /gene="Patr A"
                     /allele="Patr A*0802"
     CDS             <1..1092
                     /gene="Patr A"
                     /note="T cell/NK cell ligand"
                     /codon_start=1
                     /product="MHC class I antigen"
                     /protein_id="AAF76940.1"
                     /db_xref="GI:8571964"
                     /translation="VMAPRTLVLLLSGALALTQTWAGSHSMRYFSTSVSRPGRGEPRF
                     IAVGYVDNTQFVRFDSDAASQRMEPRAPWIEQEGPEYWQEETRNVKAHSQTDRANLGT
                     LRGYYNQSEDGSHTIQLMFGCDVGSDGRFLRGYRQDAYDGKDYIALNEDLRSWTAADM
                     AAQITQRKWEAAHAAEQRRAYLEGTCVEWLRRYLENGKETLQRTDPPKTHMTHHPISD
                     REATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEE
                     QRYTCHVQHEGLPKPLTLRWEPSSQPTIPIVGIIAGLVLLGAVITGAVVAAMMWRRKS
                     SDRKGGSYSQAASSDSAQGSDVSLTACKV"
BASE COUNT      217 a    331 c    364 g    179 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 9;  Length 1092;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||||||||||||||
Db     145 TACGTGGACAACACGCAGT 164


RESULT 10
AF179649
LOCUS       AF179649                1092 bp    mRNA    linear   PRI 19 JUN 2000
DEFINITION  Pan troglodytes MHC class I antigen (Patr A) mRNA, Patr A*0803
            allele, partial cds.
ACCESSION   AF179649
VERSION     AF179649.1  GI:8571965
KEYWORDS
SOURCE      Pan troglodytes.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1092)
  AUTHORS   Adams,E.J., Cooper,S., Thomson,G. and Parham,P.
  TITLE     Common chimpanzees have greater diversity than humans at two of the
            three highly polymorphic MHC class I genes
  JOURNAL   Immunogenetics 51 (6), 410-424 (2000)
  MEDLINE   20322476
   PUBMED   10866107
REFERENCE   2  (bases 1 to 1092)
  AUTHORS   Adams,E.J., Cooper,S., Thomson,G. and Parham,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (24 AUG 1999) Structural Biology (Stanford)/Integrative
            Biology (UC Berkeley), Stanford University/UC Berkeley, Campus
            Drive West, Stanford, CA 94305, USA
FEATURES             Location/Qualifiers
     source          1..1092
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /cell_type="BLCL"
     gene            <1..1092
                     /gene="Patr A"
                     /allele="Patr A*0803"
     CDS             <1..1092
                     /gene="Patr A"
                     /note="T cell/NK cell ligand"
                     /codon_start=1
                     /product="MHC class I antigen"
                     /protein_id="AAF76941.1"
                     /db_xref="GI:8571966"
                     /translation="VMAPRTLVLLLSGALALTQTWAGSHSMRYFSTSVSRPGRGEPRF
                     IAVGYVDNTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDEETRNVKAHSQTDRANLGT
                     LRGYYNQSEDGSHTIQIMYGCDVGSDGRFLRGYRQDAYDGKDYIALNEDLRSWTAADM
                     AAQITQRKWEAAHAAEQRRAYLEGTCVEWLRRYLENGKETLQRTDPPKTHMTHHPISD
                     REATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEE
                     QRYTCHVQHEGLPKPLTLRWEPSSQPTIPIVGIIAGLVLLGAVITGAVVAAVMWRRKS
                     SDRKGGSYSQAASSDSAQGSDVSLTACKV"
BASE COUNT      218 a    331 c    364 g    179 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 9;  Length 1092;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||||||||||||||
Db     145 TACGTGGACAACACGCAGT 164


RESULT 11
AF168404
LOCUS       AF168404                1098 bp    mRNA    linear   PRI 31 MAY 2000
DEFINITION  Pan troglodytes MHC class I antigen (Patr-A) mRNA, Patr-A*0601
            allele, complete cds.
ACCESSION   AF168404
VERSION     AF168404.1  GI:9117818
KEYWORDS    .
SOURCE      Pan troglodytes.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   de Groot,N.G., Otting,N., Arguello,R., Watkins,D.I., Doxiadis,I.G.,
            Madrigal,J.A. and Bontrop,R.E.
  TITLE     Major histocompatibility complex class I diversity in a West
            African chimpanzee population: implications for HIV research
  JOURNAL   Immunogenetics 51 (6), 493-499 (2000)
  MEDLINE   20322475
   PUBMED   10866106
REFERENCE   2  (bases 1 to 1098)
  AUTHORS   de Groot,N.G., Otting,N., Arguello,R., Watkins,D.I.,
            Doxiadis,G.G.M., Madrigal,J.A. and Bontrop,R.E.
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  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUL-1999) Immunobiology, BPRC, Lange Kleiweg 139,
            Rijswijk 2280 GH, The Netherlands
FEATURES             Location/Qualifiers
     source          1..1098
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /cell_type="transformed b cells"
                     /tissue_type="blood"
                     /note="reference animal: Brigitte"
     gene            1..1098
                     /gene="Patr-A"
                     /allele="Patr-A*0801"
     CDS             1..1098
                     /gene="Patr-A"
                     /codon_start=1
                     /product="MHC class I antigen"
                     /protein_id="AAF72785.1"
                     /db_xref="GI:8117819"
                     /translation="MAVMAPRTLVLLLSGALALTQTWAGSHSMRYFSTSVSRPGRGEP
                     RFIAVGYVDNTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDQETRSVKAGAQTYRANL
                     GTLRGYYNQSEDGSHTIQIMFGCDVGSDGRFLRGYEQLAYDGKDYIALNEDLRSWTAA
                     DMAAQITQRKWEAAHAAEQRRAYLEGTCVEWLRRYLENGKETLQRTDPPKTHMTHHPI
                     SDREATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSG
                     EEQRYTCHVQHEGLLKPLTLRWEPSSQPTIPIVGIIAGLVLLGAVITGAVVAAMMWRR
                     KSSDRKGGSYSQAASSDSAQGSDVSLTACKV"
BASE COUNT       219 a    333 c    366 g    180 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 9;  Length 1098;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||||||||||||
Db     151 TACGTGGACAACACGCAGT 169


RESULT 12
AF168405
LOCUS       AF168405                1098 bp    mRNA    linear   PRI 31-MAY 2000
DEFINITION  Pan troglodytes MHC class I antigen (Patr-A) mRNA, Patr-A*1001
            allele, complete cds.
ACCESSION   AF168405
VERSION     AF168405.1  GI:8117820
KEYWORDS    .
SOURCE      Pan troglodytes.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   de Groot,N.G., Otting,N., Arguello,R., Watkins,D.I., Doxiadis,G.G.,
            Madrigal,J.A. and Bontrop,R.E.
  TITLE     Major histocompatibility complex class I diversity in a West
            African chimpanzee population: implications for HIV research
  JOURNAL   Immunogenetics 51 (6), 398-409 (2000)
  MEDLINE   20322475
  PUBMED    10866109
REFERENCE   2  (bases 1 to 1098)
  AUTHORS   de Groot,N.G., Otting,N., Arguello,R., Watkins,D.I.,
            Doxiadis,G.G.M., Madrigal,J.A. and Bontrop,R.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUL-1999) Immunobiology, BPRC, Lange Kleiweg 139,
            Rijswijk 2299 GH, The Netherlands
FEATURES             Location/Qualifiers
     source          1..1098
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /cell_type="transformed b-cells"
                     /tissue_type="blood"
                     /note="reference animal: Brigitte"
     gene            1..1098
                     /gene="Patr-A"
                     /allele="Patr-A*1001"
     CDS             1..1098
                     /gene="Patr-A"
                     /codon_start=1
                     /product="MHC class I antigen"
                     /protein_id="AAF72786.1"
                     /db_xref="GI:8117821"
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                     RFIAVGYVDNTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDQETRSVKAGAQTYRANL
                     GTLRGYYNQSEDGSHTIQIMFGCDVGSDGRFLRGYEQHAYDGKDYIALNEDLRSWTAA
                     DMAAQITQRKWEAAHAAEQRRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAV
                     SDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSG
                     EEQRYTCHVQHEGLPKPLTLRWEPSSQPTIPIVGIIAGLVLLGAVITGAVVAAVMWRR
                     KSSDRKGGSYSQAASSDSAQGSDVSLTACKV"
BASE COUNT       220 a    331 c    365 g    182 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 9;  Length 1098;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           |||||||||||||||||||
Db     151 TACGTGGACAACACGCAGT 169


RESULT 13
HSU56825
LOCUS       HSU56825                1098 bp    mRNA    linear   PRI 24-OCT 1996
DEFINITION  Human MHC class I antigen HLA-A2 mRNA, complete cds.
ACCESSION   U56825
VERSION     U56825.1  GI:1644573
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   Szmania,S. and Baxter-Lowe,L.A.
  TITLE     Nucleotide sequence of a boxer HLA-A2 gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1098)
  AUTHORS   Szmania,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-1996) Susann Szmania, Molecular Genetics,
            Richland Memorial Hospital, 7 Richland Medical Park, Columbia, SC
            29203, USA
FEATURES             Location/Qualifiers
     source          1..1098
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /cell_type="lymphocyte"
                     /tissue_type="blood"
                     /note="Epstein-Barr transformed B-cell line"
     CDS             1..1098
                     /note="allele A2"
                     /codon_start=1
                     /product="MHC class I antigen HLA-A2"
                     /protein_id="AAB17465.1"
                     /db_xref="GI:1644574"
                     /translation="MAVMAPRTLVLLLSGALALTQTWAGSHSMRYFYTSVSRPGRGEP
                     RFIAVGYVDNTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDRETQICKAKAQTDRVSL
                     GTLRGYYNQSEAGSHTIQIMYGCDVGSDGRFLRGYRQYAYDGKDYIALKEDLRSWTAA
                     DMAAQITKRKWEAAHEAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAV
                     SDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSG
                     QEQRYTCHVQHEGLPKPLTLRWEPSSQPTIPIVGIIAGLVLLGAVITGAVVAAVMWRR
                     KSSDRKGGSYSQAASSDSAQGSDVSLTACKV"
BASE COUNT       221 a    324 c    367 g    186 t
ORIGIN

  Query Match             100.0%;  Score 19;  DB 9;  Length 1098;
  Best Local Similarity   100.0%;  Pred. No. 15;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TACGTGGACAACACGCAGT 19
           ||||||||||||||||||||
Db     151 TACGTGGACAACACGCAGT 169


RESULT 14
CHPMHC02A
LOCUS       CHPMHC02A               1269 bp    mRNA    linear   PRI 01-FEB-1995
DEFINITION  Pan paniscus (clones maa192, maa193, maa183 and maa184) MHC class I
            (A locus, 02 allele) alpha chain mRNA, complete cds.
ACCESSION   L39094
VERSION     L39094.1  GI:642083
KEYWORDS    cell surface antigen; cell surface glycoprotein; class I gene;
            integral membrane protein; major histocompatibility complex.
SOURCE      Pan paniscus (individual_isolate Matata) female cDNA to mRNA, Pan
            paniscus (individual_isolate Matata) female DNA, Pan paniscus
            (individual_isolate Matata) female DNA, and Pan paniscus
            (individual_isolate Matata) female DNA.
  ORGANISM  Pan paniscus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1269)
  AUTHORS   Lawlor,D.A., Edelson,B.I. and Parham,P.
  TITLE     MHC-A locus molecules in pygmy chimpanzees. Conservation of peptide
            pockets
  JOURNAL   Unpublished (1995)
FEATURES             Location/Qualifiers
     source          1..1269
                     /organism="Pan paniscus"
                     /isolate="Matata"
                     /db_xref="taxon:9597"
                     /clone="maa184"
                     /clone="maa192"
                     /clone="maa193"
                     /clone="maa183"
                     /sex="female"
                     /cell_line="Matata, Epstein Barr virus transformed B
                     lymphoblastoid"
     CDS             1..1098
                     /codon_start=1
                     /product="MHC class I alpha chain"
                     /protein_id="AAA61827.1"
                     /db_xref="GI:642084"
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                     GTLRGYYNQSEDGSHTIQIMYGCDVGSDGRFLRGYRQDAYDGKDYIALNEDLRSWTAA
                     DMAAQITQRKWEAAHAAEQRRAYLEGTCVEWLRRYLENGKETLQRTDPPKTHMTHHPI
                     SDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSG
                     EEQRYTCHVQHEGLLKPLILRWEPSSQPTIPIVGIIAGLVLLGAVITGAVVAAMMWRR
                     KSSDRKGGSYSQAASSDSAQGSDVSLTACKV"
     sig_peptide     1..72
     mat_peptide     73..1095
                     /product="MHC class I alpha chain"
     exon            1..73
                     /note="leader"
                     /number=1
     exon            74..343
                     /note="alpha 1"
                     /number=2
     exon            344..619
                     /note="alpha 2"
                     /number=3
     exon            620..895
                     /note="alpha 3"
                     /number=4
     exon            896..1012
                     /note="transmembrane segment"
                     /number=5
     exon            1013..1045
                     /note="cytoplasmic 1"
                     /number=6
     exon            1046..1093
                     /note="cytoplasmic 2"
                     /number=7
     exon            1094..1098
                     /note="cytoplasmic 3"
                     /number=8
BASE COUNT       254 a    379 c    411 g    226 t
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Db     151 TACGTGGACAACACGCAGT 169


RESULT 15
MMU55067
LOCUS       MMU55067                1420 bp    mRNA    linear   PRI 15-JAN-1997
DEFINITION  Macaca mulatta MHC class I HLA-G ortholog (Mamu-G*01) pseudogene
            mRNA, splice variant, partial sequence.
ACCESSION   U55067
VERSION     U55067.1  GI:1322303
KEYWORDS    .
SOURCE      Macaca mulatta.
  ORGANISM  Macaca mulatta
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            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1420)
  AUTHORS   Boyson,J.E., Iwanaga,K.K., Golos,T.G. and Watkins,D.I.
  TITLE     Identification of the rhesus monkey HLA-G ortholog, Mamu-G is a
            pseudogene
  JOURNAL   J. Immunol. 157 (12), 5426-5437 (1996)
  MEDLINE   97113331
   PUBMED   8955191
REFERENCE   2  (bases 1 to 1420)
  AUTHORS   Boyson,J.E., Iwanaga,K.K., Golos,T.G. and Watkins,D.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-1996) Jonathan E. Boyson, Pathology, Wisconsin
            Regional Primate ReSearch Center, 1220 Capitol Court, Madison, WI
            53715, USA
FEATURES             Location/Qualifiers
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ORIGIN

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Qy       1 TACGTGGACAACACGCAGT 19
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Search completed: April 15, 2003, 01:18:15
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